

GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

Run on: July 4, 2004, 19:09:46 ; Search time 3463 seconds

(without alignments)  
9624.832 Million cell updates/sec

Title: US-10-031-818b-1

Perfect score: 769  
Sequence: 1 gggatctttttaaataacc.....ggtagtttttgatattccc 769Scoring table: OLIGO NWC  
Gapop 60.0 , Gapext 60.0

Searched: 3470272 segs, 2167151695 residues

Word size: 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenBank:\*

1: gb\_ba:\*

2: gb\_htg:\*

3: gb\_in:\*

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6: gb\_ov:\*

7: gb\_ov:\*

8: gb\_ov:\*

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10: gb\_ov:\*

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12: gb\_ov:\*

13: gb\_ov:\*

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18: gb\_ov:\*

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41: gb\_ov:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	769	100.0	769	6	E52167	E52167 Novel MITE-
2	769	100.0	769	6	AX078786	AX078786 Sequence
3	769	100.0	769	6	BD013409	BD013409 Transcript
4	769	100.0	1192	6	AX078788	AX078788 Sequence
5	769	100.0	1192	6	BD013411	BD013411 Transcript
6	769	100.0	1553	6	AX078799	AX078799 Sequence
7	769	100.0	1553	6	BD013422	BD013422 Transcript
8	769	100.0	7276	8	AB089813	AB089813 Dancus ca
9	158	20.5	158	6	E52165	E52165 Novel MITE-
10	158	20.5	158	6	E52166	E52166 Novel MITE-
11	158	20.5	158	6	AX078795	AX078795 Sequence
12	158	20.5	158	6	AX078796	AX078796 Sequence
13	158	20.5	158	6	BD013418	BD013418 Transcript
14	158	20.5	158	6	BD013419	BD013419 Transcript
15	112	14.6	769	6	E52167	E52167 Novel MITE-
16	112	14.6	769	6	AX078786	AX078786 Sequence
17	112	14.6	769	6	BD013409	BD013409 Transcript
18	112	14.6	1192	6	AX078788	AX078788 Sequence
19	112	14.6	1192	6	BD013411	BD013411 Transcript
20	112	14.6	1553	6	AX078799	AX078799 Sequence
21	112	14.6	1553	6	BD013422	BD013422 Transcript
22	112	14.6	7276	8	AB089813	AB089813 Dancus ca
23	31	4.0	185272	2	AC121394	AC121394 Rattus no
24	31	4.0	209878	2	AC121394	AC121394 Rattus no
25	31	4.0	209878	2	AC121318	AC121318 Rattus no
26	31	4.0	209878	2	AC121318	AC121318 Rattus no
27	31	4.0	158	6	E52165	E52165 Novel MITE-
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35	31	3.9	110659	8	AP005691	AP005691 Oryza sat
36	31	3.9	113800	8	AC006567	AC006567 Arabidops
37	31	3.9	113800	8	AC006567	AC006567 Arabidops
38	31	3.9	128411	5	AC107365	AC107365 Dancus ca
39	31	3.9	128411	5	AC107365	AC107365 Dancus ca
40	31	3.9	139056	2	AC141691	AC141691 Apis meli
41	31	3.9	139056	2	AC141691	AC141691 Apis meli
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## ALIGNMENTS

## RESULT 1

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

E52167 Novel MITE-like factor.

E52167

E52167.1 GI:18629630

JP 2001029077-A/3.

unidentified

unclassified

unclassified

769 bp

DNA

linear

PAT 31-JAN-2002

Koyanagi, M., Koseki, Y. and Koda, T.

Novel MITE-like factor

Patent: JP 2001029077-A 3 06-FEB-2001;

YOSHIMIRO KOSEKI, SAN EI GEN FFI INC



Db 541 AATGACATTCGAAAACGTGAAATCTGAATCAGCAATTCAGCTCATATGAGTTGCAAA 600  
Qy 601 GAGGTGGCAACAGGCTGGCGCCGCTGATGTCGAAATGAGTTGCAAAAGTTGCAAC 660  
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LOCUS Transcriptional factor.  
DEFINITION BD013409  
ACCESSION BD013409.1 GI:22553723  
VERSION JP 2001086994-A/1.  
KEYWORDS unclassified  
SOURCE unclassified  
ORGANISM unclassified  
REFERENCE 1 (bases 1 to 769)  
AUTHORS Koyanagi, M., Fukuda, T., Ozeki, Y. and Koda, T.  
TITLE Transcriptional factor  
JOURNAL Patent: JP 2001086994-A 1 03-APR-2001;  
YOSHIIRO OZEKI, SAN EI GEN FFI INC  
OS Daucus carota L. cv. Kurodagosun (carrot)  
PK JP 2001086994-A/1  
PD 03-APR-2001  
PE 12-JUN-2000 JP 2000175825  
PI MIKIO KOYANAGI, TAKASHI FUKUDA, YOSHIIRO OZEKI, TAKATOSHI KODA  
PC C12N15/09, A01H5/00//C12N5/10, C12N15/00, C12N5/00 CC  
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/organism="Daucus carota L. cv. Kurodagosun FT  
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Location/Qualifiers  
1..769  
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ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 769; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 TCAATGTTTTTAAAAATACCTTTTCATAAATTTTCTTCAAAAATACGATTTGCACT 120  
Qy 121 TTGCAACCTCATTTGCAACCTTTGGCGCGCAGCCGTAAGTCCAGTGAAGTTGCA 180  
Db 121 TTGCAACCTCATTTGCAACCTTTGGCGCGCAGCCGTAAGTCCAGTGAAGTTGCA 180  
Qy 181 AAAGTTGCAATGAGTTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 240  
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Db 241 GGAAGTTGCAACAGTTGCAACTGCAATTTGCAACTGCAACTGCAACTGCAACTG 300  
Qy 301 AAAAGTTGCAATGAGTTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTG 360

Db 301 AAAAGTTGCAATGAGTTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTG 360  
Qy 361 ATGTGTGCCCCCTGGCGCGCCGCTGATGTCGAAATGAGTTGCAAAAGTTGCAAC 420  
Db 361 ATGTGTGCCCCCTGGCGCGCCGCTGATGTCGAAATGAGTTGCAAAAGTTGCAAC 420  
Qy 421 CAAGTGAATGCAATGATGCAATGATGCAATGATGCAATGATGCAATGATGCAAT 480  
Db 421 CAAGTGAATGCAATGATGCAATGATGCAATGATGCAATGATGCAATGATGCAAT 480  
Qy 481 GTTTTGAATGTCATTTTGAATGATATATATATATATATATATATATATATATAT 540  
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RESULT 4  
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LOCUS Sequence 3 from Patent WO0105986.  
DEFINITION AX078788  
ACCESSION AX078788  
VERSION AX078788.1 GI:13158405  
KEYWORDS  
SOURCE Daucus carota (carrot)  
ORGANISM Daucus carota  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; Campanulids; Apiales; Apiaceae; Apioidae; Scandiceae;  
Daucineae; Daucus.  
REFERENCE 1  
AUTHORS Ozeki, Y., Oyanagi, M., Fukuda, T. and Koda, T.S.  
TITLE Mites-like element and transcriptional activation element  
JOURNAL Patent: WO 0105986-A 3 25-JAN-2001;  
SAN-EI GEN F.F.I., INC. (JP) ; Ozeki, Yoshihiro (JP)  
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/mol\_type="unassigned DNA";  
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/note="L. cv. Kurodagosun"

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 769; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 TCAATGTTTTTAAAAATACCTTTTCATAAATTTTCTTCAAAAATACGATTTGCACT 120  
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/db_xref="taxon:32644"

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Tue Jul 6 09:07:33 2004

us-10-031-818b-1.01i.rge

Page 5

AUTHORS Ozeki,Y., Oyamagi,M., Fukuda,T. and Koda,T.S.  
TITLE Mites-like element and transcriptional activation element  
JOURNAL Patent: WO 0105986-A 14 25-JAN-2001;  
SAN-EI GEN F.F.I., INC. (JPN) ; Ozeki, Yoshihiro (JP)

FEATURES Location/Qualifiers  
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Query Match 100.0%; Score 769; DB 6; Length 1553;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 769; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TCATGCTTTTAAATAACCTTTTCATTAATTTTTCATAAATAACGATTGCACT 120
DB 826 TCATGCTTTTAAATAACCTTTTCATTAATTTTTCATAAATAACGATTGCACT 885
QY 121 TTTCGACCTCATTTTGCACCTTTGGGCGCGCAGCCGTAAAGTTGCCAGTGTGCA 180
DB 886 TTTCGACCTCATTTTGCACCTTTGGGCGCGCAGCCGTAAAGTTGCCAGTGTGCA 945
QY 181 AAAGTGCATAATGAGTTTGAATAAGTTGCAAAATGAGTTGCAAAAGTTCAATAAAT 240
DB 946 AAAGTGCATAATGAGTTTGAATAAGTTGCAAAATGAGTTGCAAAAGTTCAATAAAT 1005
QY 241 GGAAGTTGCAACAGTTGCACTGCAATGTCATAGTTCAACTGAAATCTGTAAGTTC 300
DB 1006 GGAAGTTGCAACAGTTGCACTGCAATGTCATAGTTCAACTGAAATCTGTAAGTTC 1065
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DB 1066 AAAAGTTGCAATGAGTTGCACTGCAATGTCATAGTTGCAAAAGTTGTAAGCAACGAGT 1125
QY 361 ATGCTGTCCTCCCTGGCGGCGCGCTTGAATTAACAATGAAATCAATGCAATCATATG 420
DB 1126 ATGCTGTCCTCCCTGGCGGCGCGCTTGAATTAACAATGAAATCAATGCAATCATATG 1185
QY 421 CAACGTAAATCAACTATATGCAATCAATATGCAATTAACAATCCGATTTCAAGTTCA 480
DB 1186 CAACGTAAATCAACTATATGCAATCAATATGCAATTAACAATCCGATTTCAAGTTCA 1245
QY 481 GTTTCGAATGTCATTTTGAATTCATATATATATATATATATATATATATATATATG 540
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DB 1366 GAGGTTCGAAACGCGTGGCGCGCTGATGTTGCAAAATGAGTTGCAAAAGTTGCAAA 1425
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RESULT 7  
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DEFINITION Transcriptional factor.

ACCESSION BD013422  
VERSION BD013422.1 GI:22553736  
KEYWORDS JP 2001086994-A/14.  
SOURCE unidentified  
ORGANISM unidentified

REFERENCE 1 (bases 1 to 1553)  
AUTHORS Koyanagi,M., Fukuda,T., Ozeki,Y. and Koda,T.  
TITLES Transcriptional factor  
JOURNAL Patent: JP 2001086994-A 14 03-APR-2001;  
YOSHIIRO OZEKI,SAN EI GEN FFI INC

COMMENT OS Daucus carota L.cv. Kurodagosun (carrot)  
PN JP 2001086994-A/14  
PD 03-APR-2001  
PF 12-JUN-2000 JP 2000175825  
PI MIKIRO KOYANAGI,TAKASHI FUKUDA,YOSHIIRO OZEKI,TAKATOSHI KODA  
PC C12N5/09 A01H5/00/C12N5/10,C12N5/00,C12N5/00 CC  
Transcriptional factor

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Location/Qualifiers (carrot)

FEATURES location/Qualifiers  
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#### ORIGIN

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QY 61 TCATGCTTTTAAATAACCTTTTCATTAATTTTTCATAAATAACGATTGCACT 120
DB 826 TCATGCTTTTAAATAACCTTTTCATTAATTTTTCATAAATAACGATTGCACT 885
QY 121 TTTCGACCTCATTTTGCACCTTTGGGCGCGCAGCCGTAAAGTTGCCAGTGTGCA 180
DB 886 TTTCGACCTCATTTTGCACCTTTGGGCGCGCAGCCGTAAAGTTGCCAGTGTGCA 945
QY 181 AAAGTGCATAATGAGTTTGAATAAGTTGCAAAATGAGTTGCAAAAGTTCAATAAAT 240
DB 946 AAAGTGCATAATGAGTTTGAATAAGTTGCAAAATGAGTTGCAAAAGTTCAATAAAT 1005
QY 241 GGAAGTTGCAACAGTTGCACTGCAATGTCATAGTTCAACTGAAATCTGTAAGTTC 300
DB 1006 GGAAGTTGCAACAGTTGCACTGCAATGTCATAGTTCAACTGAAATCTGTAAGTTC 1065
QY 301 AAAAGTTGCAATGAGTTGCACTGCAATGTCATAGTTGCAAAAGTTGTAAGCAACGAGT 360
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DB 1126 ATGCTGTCCTCCCTGGCGGCGCGCTTGAATTAACAATGAAATCAATGCAATCATATG 1185
QY 421 CAACGTAAATCAACTATATGCAATCAATATGCAATTAACAATCCGATTTCAAGTTCA 480
DB 1186 CAACGTAAATCAACTATATGCAATCAATATGCAATTAACAATCCGATTTCAAGTTCA 1245
QY 481 GTTTCGAATGTCATTTTGAATTCATATATATATATATATATATATATATATATATG 540
DB 1246 GTTTCGAATGTCATTTTGAATTCATATATATATATATATATATATATATATATG 1305
QY 541 AATGCAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAAT 600
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OY		661	AGTAATTTTGAATAAAGATTATTAAGAAAAGTAGATTGTAATTTCC	720
Dd		1426	AGTAATTTTGAATAAAGATTATTAAGAAAAGTAGATTGTAATTTCC	1485
OY		721	TATTTTGAAAAACAATTAAGAAGAGTAGATTGTAATTTCC	769
Dd		1486	TATTTTGAAAAACAATTAAGAAGAGTAGATTGTAATTTCC	1534
RESULT B				
AB089813				
LOCUS				
DEFINITION	Daucus carota gDcPAL3 gene for phenylalanine ammonia-lyase,			
VERSION	complete cds.			
KEYWORDS:	AB089813.1 GI:28316385			
ORGANISM	Daucus carota (carrot)			
SOURCE	Daucus carota Euxarietia; Vitridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatocytas; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Apiales; Apiaceae; Apioideae; Scandiceae;			
REFERENCE				
AUTHORS	Daucines; Daucus.			
TITLE	1 Ozeki,Y., Chikagawa,Y., Kinura,S., Sch,H., Maeda,K., Portnitsiwong,M., Kato,M., Akimoto,H., Oyanagi,M., Fukuda,T., Koda,T., Itoh,Y., Yamada,A., Ueno,H. and Takeda,J. Putative cis-elements in the promoter region of phenylalanine ammonia-lyase gene of carrot involved in anthocyanin biosynthetic pathway Unpublished 2 (bases 1 to 7276) Ozeki,Y., Chikagawa,Y., Kinura,S., Maeda,K., Oyanagi,M., Fukuda,T., Koda,T., Itoh,Y., Yamada,A. and Takeda,J. Direct Submission Submitted (13-AUG-2002) Yoshihiro Ozeki, Tokyo University of Agriculture and Technology, Department of Biotechnology; Naka-chou 2-24-16, Koganei, Tokyo 184-8588, Japan (E-mail:ozeki@cc.tuat.ac.jp, Tel:81-42-388-7239, Fax:81-42-388-7239)			
JOURNAL				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
FEATURES				
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Query Match	100.0%	Score 769	DB 8	Length 7276	
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QY	61	TCATGTGTTTAAAAAATACCTTTTCATTAATTTTTTTTTCAAAAATACGATTGCACT	120		
DB	1443	TCATGTGTTTAAAAAATACCTTTTCATTAATTTTTTTTTCAAAAATACGATTGCACT	1502		
QY	121	TTTGCAACTCATTTTGCACCTTGGGGCGCGCCGACCCGTAAAGTTGCCAGTGGTTC	180		
DB	1503	TTTGCAACTCATTTTGCACCTTGGGGCGCGCCGACCCGTAAAGTTGCCAGTGGTTC	1562		
QY	181	AAAGTGCAAATGAGTTGTAAAGTTGCAAATGAGTGCAAAAGTTGCAAATATAAT	240		
DB	1563	AAAGTGCAAATGAGTTGTAAAGTTGCAAATGAGTGCAAAAGTTGCAAATATAAT	1622		
QY	241	GGAAGTTGCACAGTTGCACCTGCATTTGCACTAGTTCACTGAAAACCTGTAGTTC	300		
DB	1623	GGAAGTTGCACAGTTGCACCTGCATTTGCACTAGTTCACTGAAAACCTGTAGTTC	1682		
QY	301	AAAAGTGCAAATGAGTTGCACCTAAATGCACCTGAAAACCTGTAGTAAACAAGATGT	360		
DB	1683	AAAAGTGCAAATGAGTTGCACCTAAATGCACCTGAAAACCTGTAGTAAACAAGATGT	1742		
QY	361	ATGCTGTCCTCCCTGGCGGGCGCGTTAGATTGCAATAGATCAACTGAATGCATCATATG	420		
DB	1743	ATGCTGTCCTCCCTGGCGGGCGCGTTAGATTGCAATAGATCAACTGAATGCATCATATG	1802		
QY	421	CAACGTGAATCAACTATATGCATCATATATGCAATTCGAATCTGATTTCAAGTTCCA	480		
DB	1803	CAACGTGAATCAACTATATGCATCATATATGCAATTCGAATCTGATTTCAAGTTCCA	1862		
QY	481	GTTTTCGAATGTCATTTTCGAAATCGATATATATATATATATATATATGATTCGAA	540		
DB	1863	GTTTTCGAATGTCATTTTCGAAATCGATATATATATATATATATATATGATTCGAA	1922		
QY	541	AATGACATTCGAAAACCTGGAACCTTGAATCAGGAATTCAGCTGCATATGAAGTTGCAAA	600		
DB	1923	AATGACATTCGAAAACCTGGAACCTTGAATCAGGAATTCAGCTGCATATGAAGTTGCAAA	1982		
QY	601	GAGGTTCGACACCGCTGCGCGCCCTGTGTTGTCGAAATGAGCTTCGAAAAGTTGCAAA	660		
DB	1983	GAGGTTCGACACCGCTGCGCGCCCTGTGTTGTCGAAATGAGCTTCGAAAAGTTGCAAA	2042		
QY	661	AGTATTTTGGAAAAAAGATTTTATGAAAAGTATTTTAAATAATATTCGAAGGTAG	720		
DB	2043	AGTATTTTGGAAAAAAGATTTTATGAAAAGTATTTTAAATAATATTCGAAGGTAG	2102		
QY	721	TATTTTGGAAAACATATAAGAAAGGTAGTATTTTGTAGATTTTCC	769		
DB	2103	TATTTTGGAAAACATATAAGAAAGGTAGTATTTTGTAGATTTTCC	2151		



ORGANISM unidentified  
unclassified.  
REFERENCE 1 (bases 1 to 158)  
AUTHORS Koyanagi, M., Koseki, Y. and Koda, T.  
TITLE Novel MITE-like factor  
JOURNAL Patent: JP 2001029077-A 1 06-FEB-2001;  
YOSHIIRO KOSEKI, SAN EI GEN FFI INC  
OS Daucus carota L. cv. Kurodagosun (Carrot)  
PN JP 2001029077-A/1  
PD 06-FEB-2001  
PF 21-JUL-1999 JP 1999206316  
PR MIKIRO KOYANAGI, YOSHIIRO KOSEKI, TAKATOSHI KODA PC  
C12N15/09//A01H1/00, C12N5/10, (C12N15/09, C12R1:91), C12N15/00, PC  
C12N5/00,  
PC (C12N15/00, C12R1:91)  
CC  
FH Key Location/Qualifiers  
FT source 1. 158  
/organism="Daucus carota L. cv. Kurodagosun"  
/location/Qualifiers  
1. 158  
/organism="unclassified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

ORIGIN  
Query Match 20.5%; Score 158; DB 6; Length 158;  
Best Local Similarity 100.0%; Pred. No. 9.6e-71;  
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGATCTTTTAAAAATACCCATCTGTAATATTTTAAAAATACCACTTTT 60  
DB 1 GGGATCTTTTAAAAATACCCATCTGTAATATTTTAAAAATACCACTTTT 60  
QY 61 TCATGTCTTTTAAAAATACCTTTTCATTAATTTTTCACAAAATACGATTGCACT 120  
DB 61 TCATGTCTTTTAAAAATACCTTTTCATTAATTTTTCACAAAATACGATTGCACT 120  
QY 121 TTGCAACCTCATTTGCAACCTTTGGGCGCGGACCGCT 158  
DB 121 TTGCAACCTCATTTGCAACCTTTGGGCGCGGACCGCT 158

RESULT 10  
E52166 158 bp DNA linear PAT 31-JAN-2002  
LOCUS E52166  
DEFINITION Novel MITE-like factor.  
ACCESSION E52166  
VERSION E52166.1 GI:18629629  
KEYWORDS JP 2001029077-A/2.  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.  
REFERENCE 1 (bases 1 to 158)  
AUTHORS Koyanagi, M., Koseki, Y. and Koda, T.  
TITLE Novel MITE-like factor  
JOURNAL Patent: JP 2001029077-A 2 06-FEB-2001;  
YOSHIIRO KOSEKI, SAN EI GEN FFI INC  
OS Daucus carota L. cv. Kurodagosun (Carrot)  
PN JP 2001029077-A/2  
PD 06-FEB-2001  
PF 21-JUL-1999 JP 1999206316  
PR MIKIRO KOYANAGI, YOSHIIRO KOSEKI, TAKATOSHI KODA PC  
C12N15/09//A01H1/00, C12N5/10, (C12N15/09, C12R1:91), C12N15/00, PC  
C12N5/00,  
PC (C12N15/00, C12R1:91)  
CC  
FH Key Location/Qualifiers  
FT source 1. 158  
/organism="Daucus carota L. cv. Kurodagosun"  
/location/Qualifiers  
1. 158  
/organism="unclassified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

FEATURES (Carrot).  
Location/Qualifiers  
1. 158  
/organism="unclassified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

ORIGIN  
Query Match 20.5%; Score 158; DB 6; Length 158;  
Best Local Similarity 100.0%; Pred. No. 9.6e-71;  
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 612 ACGGCTGGCGCGCGCTGATGTGCAAAATAGAGTTGCAAAAGTTGCAAAAGATTGGA 671  
DB 1 ACGGCTGGCGCGCGCTGATGTGCAAAATAGAGTTGCAAAAGTTGCAAAAGATTGGA 60  
QY 672 AAAAAAGATTTCAGAAAAGGTTATTTTAAAAATATCTGAAAAGTTAGATTTTGAAA 731  
DB 61 AAAAAAGATTTCAGAAAAGGTTATTTTAAAAATATCTGAAAAGTTAGATTTTGAAA 120  
QY 732 ACAATTAAGAAAAGTTAGTTGTTTTCATATTTCC 769  
DB 121 ACAATTAAGAAAAGTTAGTTGTTTTCATATTTCC 158

RESULT 11  
AX078795 158 bp DNA linear PAT 22-FEB-2001  
LOCUS AX078795  
DEFINITION Sequence 10 from Patent WO0105986.  
ACCESSION AX078795  
VERSION AX078795.1 GI:13158412  
KEYWORDS  
SOURCE Daucus carota (carrot)  
ORGANISM Daucus carota  
Buxaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; campanulids; Apiales; Apiaceae; Apioidae; Scandiceae;  
Daucinae; Daucus.  
REFERENCE 1  
AUTHORS Ozeki, Y., Oyanagi, M., Fukuda, T. and Koda, T. S.  
TITLE Mites-like element and transcriptional activation element  
JOURNAL Patent: WO 0105986-A 10 25-JAN-2001;  
SAN-EI GEN F.F.I., INC. (JP) ; Ozeki, Yoshihiro (JP)  
LOCATION/Qualifiers  
1. 158  
/organism="Daucus carota"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:4039"  
/note="L. cv. Kurodagosun"

ORIGIN  
Query Match 20.5%; Score 158; DB 6; Length 158;  
Best Local Similarity 100.0%; Pred. No. 9.6e-71;  
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGATCTTTTAAAAATACCCATCTGTAATATTTTAAAAATACCACTTTT 60  
DB 1 GGGATCTTTTAAAAATACCCATCTGTAATATTTTAAAAATACCACTTTT 60  
QY 61 TCATGTCTTTTAAAAATACCTTTTCATTAATTTTTCACAAAATACGATTGCACT 120  
DB 61 TCATGTCTTTTAAAAATACCTTTTCATTAATTTTTCACAAAATACGATTGCACT 120  
QY 121 TTGCAACCTCATTTGCAACCTTTGGGCGCGGACCGCT 158  
DB 121 TTGCAACCTCATTTGCAACCTTTGGGCGCGGACCGCT 158

RESULT 12  
AX078796 158 bp DNA linear PAT 22-FEB-2001  
LOCUS AX078796  
DEFINITION Sequence 11 from Patent WO0105986.  
ACCESSION AX078796

VERSION AX078796.1 GI:13158413  
 KEYWORDS  
 SOURCE Daucus carota (carrot)  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eudicotyledons; Magnoliophyta (eudicotyledons); core eudicotyledons; asterids; campanulids; Apiales; Apiaceae; Apioideae; Scandiceae; Dascinae; Daucus.

REFERENCE  
 AUTHORS Ozeki,Y., Oyanagi,M., Fukuda,T. and Koda,T.S.  
 TITLE Mites-like element and transcriptional activation element  
 JOURNAL Patent: WO 0105986-A 11 25-JAN-2001  
 SAN-EI GEN F.F.I., INC. (JP) ; Ozeki, Yoshihiro (JP)

FEATURES  
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 /organism="Daucus carota"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:4039"  
 /note="L.cv.Kurodagosun"

## ORIGIN

Query Match 20.5%; Score 158; DB 6; Length 158;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-71;  
 Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 612 ACGGCTGGCGCCCTGTAGTTCGCAATGAGTTGCAAAAGTTCGCAACAGTATTTTGA 671  
 DB 1 ACGGCTGGCGCCCTGTAGTTCGCAATGAGTTGCAAAAGTTCGCAACAGTATTTTGA 60  
 QY 672 AAAAAAGTTTATGAAAAAGGTATTTTAAATATTTCTGAAAGTATTTTGA 731  
 DB 61 AAAAAAGTTTATGAAAAAGGTATTTTAAATATTTCTGAAAGTATTTTGA 120  
 QY 732 ACAATTAAGAAAAAGGTAGTATTTTGTAGATTTCC 769  
 DB 121 ACAATTAAGAAAAAGGTAGTATTTTGTAGATTTCC 158

RESULT 13  
 BD013418  
 LOCUS BD013418 158 bp DNA linear PAT 27-AUG-2002  
 DEFINITION Transcriptional factor.  
 ACCESSION BD013418.1 GI:22553732  
 VERSION JP 2001086994-A/10.  
 KEYWORDS unclassified  
 SOURCE unclassified  
 ORGANISM unclassified

REFERENCE  
 1 (bases 1 to 158)  
 AUTHORS Koyanagi,M., Fukuda,T., Ozeki,Y. and Koda,T.  
 TITLE Transcriptional factor  
 JOURNAL Patent: JP 2001086994-A 10 03-APR-2001;  
 YOSHIHIRO OZEKI,SAN EI GEN FFI INC  
 OS Daucus carota L.cv.Kurodagosun (carrot)  
 PN JP 2001086994-A/10  
 PD 03-APR-2001  
 PE 12-JUN-2000 JP 2000175825  
 PI MIKIO KOYANAGI,TAKASHI FUKUDA,YOSHIHIRO OZEKI,TAKATOSHI KODA  
 PC C12N15/09,A01H5/00//C12N5/10,C12N15/00,C12N5/00 CC  
 FT Transcriptional factor  
 FH Key  
 FT source  
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 /organism="Daucus carota L.cv.Kurodagosun"  
 /db\_xref="taxon:32644"

FEATURES  
 Source  
 1..158  
 Location/Qualifiers  
 (carrot);

## FEATURES

Query Match 20.5%; Score 158; DB 6; Length 158;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-71;

Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGATCTTTTAAAAAACCACATCTGTAAATATTTTAAAAATACATCATCTTTT 60  
 DB 1 GGGATCTTTTAAAAAACCACATCTGTAAATATTTTAAAAATACATCATCTTTT 60  
 QY 61 TCAATGTTTAAAAATACCTTTTCATTAATTTTTCGAAATATGACATTTGCACT 120  
 DB 61 TCAATGTTTAAAAATACCTTTTCATTAATTTTTCGAAATATGACATTTGCACT 120  
 QY 121 TTTCGAACCTCATTTGCAACCTTGGCGGCGACCGCT 158  
 DB 121 TTTCGAACCTCATTTGCAACCTTGGCGGCGACCGCT 158

## RESULT 14

BD013419  
 LOCUS BD013419 158 bp DNA linear PAT 27-AUG-2002  
 DEFINITION Transcriptional factor.  
 ACCESSION BD013419.1 GI:22553733  
 VERSION JP 2001086994-A/11.  
 KEYWORDS unclassified  
 SOURCE unclassified  
 ORGANISM unclassified

REFERENCE  
 1 (bases 1 to 158)  
 AUTHORS Koyanagi,M., Fukuda,T., Ozeki,Y. and Koda,T.  
 TITLE Transcriptional factor  
 JOURNAL Patent: JP 2001086994-A 11 03-APR-2001;  
 YOSHIHIRO OZEKI,SAN EI GEN FFI INC  
 OS Daucus carota L.cv.Kurodagosun (carrot)  
 PN JP 2001086994-A/11  
 PD 03-APR-2001  
 PE 12-JUN-2000 JP 2000175825  
 PI MIKIO KOYANAGI,TAKASHI FUKUDA,YOSHIHIRO OZEKI,TAKATOSHI KODA  
 PC C12N15/09,A01H5/00//C12N5/10,C12N15/00,C12N5/00 CC  
 FT Transcriptional factor  
 FH Key  
 FT source  
 1..158  
 /organism="Daucus carota L.cv.Kurodagosun"  
 /db\_xref="taxon:32644"

FEATURES  
 Source  
 1..158  
 Location/Qualifiers  
 (carrot);

## ORIGIN

Query Match 20.5%; Score 158; DB 6; Length 158;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-71;  
 Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 612 ACGGCTGGCGCCCTGTAGTTCGCAATGAGTTGCAAAAGTTCGCAACAGTATTTTGA 671  
 DB 1 ACGGCTGGCGCCCTGTAGTTCGCAATGAGTTGCAAAAGTTCGCAACAGTATTTTGA 60  
 QY 672 AAAAAAGTTTATGAAAAAGGTATTTTAAATATTTCTGAAAGTATTTTGA 731  
 DB 61 AAAAAAGTTTATGAAAAAGGTATTTTAAATATTTCTGAAAGTATTTTGA 120  
 QY 732 ACAATTAAGAAAAAGGTAGTATTTTGTAGATTTCC 769  
 DB 121 ACAATTAAGAAAAAGGTAGTATTTTGTAGATTTCC 158

## RESULT 15

ES2167/c  
 LOCUS ES2167 769 bp DNA linear PAT 31-JAN-2002  
 DEFINITION Novel MITE-like factor.  
 ACCESSION ES2167  
 VERSION ES2167.1 GI:18629630  
 KEYWORDS unclassified  
 SOURCE unclassified



## ORGANISM

unidentified

unclassified.

REFERENCE  
1 (bases 1 to 769)  
AUTHORS  
Koyanagi, M., Koseki, Y. and Kodai, T.  
TITLE  
Novel MITE-like factor  
JOURNAL  
Patent: JP 2001029077-A 3 06-FEB-2001;

## COMMENT

YOSHIHIRO KOSEKI, SAN EI GEN FFI INC  
OS  
Daucus carota L. cv. Kurodagosun (Carrot)  
PN  
JP 2001029077-A/3  
PD  
06-FEB-2001  
PF  
21-JUL-1999 JP 1999206316

PR  
MIXIKO KOYANAGI, YOSHIHIRO KOSEKI, TAKAOSHI KODA PC  
C12N15/09//A01H1/00, C12N5/10, (C12N15/09, C12R1:91), C12N15/00, PC  
C12N5/00,  
PC  
(C12N15/00, C12R1:91)

## FEATURES

source

location/Qualifiers

1..769

/organism="unidentified"

/mol\_type="genomic DNA"

/db\_xref="taxon:32644"

## ORIGIN

Query Match

14.6%; Score 112; DB 6; Length 769;

Best Local Similarity 100.0%; Pred. No. 7.1e-47;

Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	463	TCCGATTTCAAGTCCAGTTTTCGAAATGATTTTCGAAATGATATATATATATAT	522
DB	574	TCCGATTTCAAGTCCAGTTTTCGAAATGATTTTCGAAATGATATATATATATAT	515
OY	523	ATAATATGATTTTGAATGACATGCAATGCAATGCAATGCAATGCAATGCAATGCA	574
DB	514	ATAATATGATTTTGAATGACATGCAATGCAATGCAATGCAATGCAATGCAATGCA	463

Search completed: July 4, 2004, 23:13:24

Job time : 3465 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

CM nucleic - nucleic search, using sw model

Run on: July 4, 2004, 17:12:11 ; Search time 407 Seconds  
(without alignments)  
8026.694 Million cell updates/sec

Title: US-10-031-818b-1

Sequence: 1 99gatcttttaaaataacc.....ggtagtttgtagattccc 769

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size: 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database: N\_Geneseq\_290an04:\*

1: geneeqn1980s:\*\n2: geneeqn1990s:\*\n3: geneeqn2000s:\*\n4: geneeqn2001s:\*\n5: geneeqn2001bs:\*\n6: geneeqn2002s:\*\n7: geneeqn2003as:\*\n8: geneeqn2003bs:\*\n9: geneeqn2003cs:\*\n10: geneeqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	769	100.0	769	4	AAFS6291
2	769	100.0	1192	4	AAFS6291 MITR-like
3	769	100.0	1543	4	AAFS6293
4	158	20.5	158	4	AAFS6295
5	158	20.5	158	4	AAFS6294
6	112	14.6	769	4	AAFS6291
7	112	14.6	1192	4	AAFS6293
8	112	14.6	1543	4	AAFS6298
9	30	3.9	158	4	AAFS6294
10	29	3.8	158	4	AAFS6295
11	29	3.8	2717	4	AB121958
12	29	3.8	2717	4	AB121958
13	28	3.6	466	3	ABN81058
14	28	3.6	466	3	ABN81058
15	28	3.6	3571	4	AB127372
16	28	3.6	3571	4	AB127372
17	28	3.6	9989	4	AB103494
18	28	3.6	9989	4	AB103494
19	27	3.5	521	6	ABQ29481
20	27	3.5	521	6	ABQ29481
21	27	3.5	521	6	ABQ29480
22	27	3.5	521	6	ABQ29480
23	27	3.5	756	6	ABQ29413

C	24	27	3.5	756	6	ABQ29413	Abq29413 Oligonuc1
C	25	27	3.5	756	6	ABQ29412	Abq29412 Oligonuc1
C	26	27	3.5	756	6	ABQ29412	Abq29412 Oligonuc1
C	27	27	3.5	3528	2	AAT31824	Aat31824 Tomato pz
C	28	27	3.5	3528	2	AAT31824	Aat31824 Tomato pz
C	29	27	3.5	3528	2	AAT48816	Aat48816 Calgene L
C	30	27	3.5	3528	2	AAT48816	Aat48816 Calgene L
C	31	27	3.5	3528	2	AB221971	Ab221971 Plasmid p
C	32	27	3.5	3528	2	AB221971	Ab221971 Plasmid p
C	33	27	3.5	4383	2	AAQ10263	Aaq10263 P2130 con
C	34	27	3.5	4383	2	AAQ10263	Aaq10263 P2130 con
C	35	27	3.5	4383	2	AAQ10319	Aaq10319 Calgene L
C	36	27	3.5	4383	2	AAQ10319	Aaq10319 Calgene L
C	37	27	3.5	4383	2	AAQ35143	Aaq35143 Calgene L
C	38	27	3.5	4383	2	AAQ35143	Aaq35143 Calgene L
C	39	27	3.5	4383	2	AAQ34941	Aaq34941 Calgene L
C	40	27	3.5	4383	2	AAQ34941	Aaq34941 Calgene L
C	41	27	3.5	4948	4	AB115082	Ab115082 Drosophill
C	42	27	3.5	4948	4	AB115082	Ab115082 Drosophill
C	43	27	3.5	6526	6	AB134236	Ab134236 Human imm
C	44	27	3.5	6526	6	AB134236	Ab134236 Human imm
C	45	27	3.5	6526	6	ABN80306	Abn80306 Human Che

#### ALIGNMENTS

RESULT 1	AAFS6291	standard; DNA; 769 BP.
ID	AAFS6291	standard; DNA; 769 BP.
XX	AAFS6291;	
AC	18-APR-2001	(first entry)
XX	MTF-like element 5' terminal inverted repeat sequence.	
DE	Miniature inverted repeat transposable element; MITE; duplication;	
XX	regulate; ds.	
KM	Daucus carota.	
XX	WO200105986-A2.	
XX	25-JAN-2001.	
PD	19-JUL-2000; 2000WO-JP004837.	
PF	21-JUL-1999; 99JP-00206316.	
XX	21-JUL-1999; 99JP-00206320.	
PR	12-JUN-2000; 2000JP-00175825.	
PA	(SANE-) SAN-EI GEN FPI INC.	
XX	(OZEK-) OZEKI Y.	
FI	Ozeeki Y, Oyanagi M, Fukuda T, Koda T;	
XX	WP1; 2001-147351/15.	
DR	Novel miniature inverted-repeat transposable element (MITR)-like element	
PT	useful for constructing transgene expression cassette for stably creating	
PT	genetically engineered organisms capable of expression of transgene.	
XX	Claim 4; Page 98-99; 104p; English.	
PS	The present invention relates to a miniature inverted-repeat transposable	
CC	element (MITR)-like element capable of causing duplication of a target	
CC	sequence at the site of its insertion in a genomic gene. The invention is	
CC	useful for causing expression of a transgene in a plant. It can also be	
CC	used for inducing or regulating the expression in a plant of the gene	
CC	introduced	
XX	Sequence 769 BP; 277 A; 113 C; 141 G; 238 T; 0 U; 0 Other;	



Db 939 AATGACATTCGAAAACCTGAACTTGAATCAGGAATTCAGTCATATGAAGTTGCAAA 998  
Qy 601 GAGGTTCGACACGCGCTGGCGCCGCTAGTTGCAAAATGAGGTTCGAAAAGTTGCAAC 660  
Db 999 GAGGTTCGACACGCGCTGGCGCCGCTAGTTGCAAAATGAGGTTCGAAAAGTTGCAAC 1058  
Qy 661 AGTATTTTGAAGAAAAGATTTTATGAAAAGATTTTAAATAATTTCTGGAAGTTAG 720  
Db 1059 AGTATTTTGAAGAAAAGATTTTATGAAAAGATTTTAAATAATTTCTGGAAGTTAG 1118  
Qy 721 TATTTTGAAGAAAAGATTTTATGAAAAGATTTTCTGATTTCC 769  
Db 1119 TATTTTGAAGAAAAGATTTTATGAAAAGATTTTCTGATTTCC 1167

RESULT 3  
ID AAF56298 standard; DNA; 1543 BP.  
XX AAF56298;  
AC AAF56298;  
XX 18-APR-2001 (first entry)  
XX IS2 element sequence #5.  
DE IS2 element sequence #5.  
XX Miniature inverted repeat transposable element; MITE; duplication;  
XX regulate; IS2; ds.  
XX Daucus carota.  
OS WO200105986-A2.  
XX 25-JAN-2001.  
PD 19-JUL-2000; 2000WO-JP004837.  
XX 21-JUL-1999; 99JP-00206316.  
XX 21-JUL-1999; 99JP-00206320.  
PR 12-JUN-2000; 2000JP-00175825.  
XX (SAME-) SAN-EI GEN FFI INC.  
PA (OZEK/) OZEKI Y.  
XX Ozeki Y, Oyanagi M, Fukuda T, Koda T,  
XX WPI; 2001-147351/15.  
DR Novel, miniature inverted-repeat transposable element (MITE)-like element  
PT useful for constructing transgene expression cassette for stably creating  
ET genetically engineered organisms capable of expression of transgene.  
XX  
PS Disclosure; Page 103-104; 104pp; English.  
XX  
CC The present invention relates to a miniature inverted-repeat transposable  
CC element (MITE)-like element capable of causing duplication of a target  
CC sequence at the site of its insertion in a genomic gene. The invention is  
CC useful for causing expression of a transgene in a plant. It can also be  
CC used for inducing or regulating the expression in a plant of the gene  
CC introduced  
XX  
SQ Sequence 1543 BP; 569 A; 244 C; 214 G; 516 T; 0 U; 0 Other;

Query Match 100.0%; Score 769; DB 4; Length 1543;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 769; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAATCTTTTAAATAATCCATCGTAAATTAATTTTAAATAATCCATCTTTT 60  
Db 756 GGAATCTTTTAAATAATCCATCGTAAATTAATTTTAAATAATCCATCTTTT 815  
Qy 61 TCAATGTTTTAAATAATCCTTTTCAATAATTTTCTTCAATAATGATTTGCACT 120

Db 816 TCAATGTTTTAAATAATCCTTTTCAATAATTTTCTTCAATAATGATTTGCAACT 875  
Qy 121 TTTCGAACCTCATTTGCAACCTTGGGCGGCGACCGCTAAAGTTGCGAGTTGCA 180  
Db 876 TTTCGAACCTCATTTGCAACCTTGGGCGGCGACCGCTAAAGTTGCGAGTTGCA 935  
Qy 181 AAATTTGCAATGAGTTTGTAAAGTTGCAAAATGAGTTGCAAAAGTTGCAAAAT 240  
Db 936 AAATTTGCAATGAGTTTGTAAAGTTGCAAAATGAGTTGCAAAAGTTGCAAAAT 995  
Qy 241 GGAAGTTGCAACAGTTGCAACCTGCAATGCAATGCAATGCAATGCAATGCAATG 300  
Db 996 GGAAGTTGCAACAGTTGCAACCTGCAATGCAATGCAATGCAATGCAATGCAATG 1055  
Qy 301 AAAGTTGCAATGAGTTGCAACCTGCAATGCAATGCAATGCAATGCAATGCAATG 360  
Db 1056 AAAGTTGCAATGAGTTGCAACCTGCAATGCAATGCAATGCAATGCAATGCAATG 1115  
Qy 361 ATGTTGTCCTTGGCGGCGGCGCTTGAATTAACATGAAATCACTGAAATGCAATG 420  
Db 1116 ATGTTGTCCTTGGCGGCGGCGCTTGAATTAACATGAAATCACTGAAATGCAATG 1175  
Qy 421 CAATGAAATCACTGAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 480  
Db 1176 CAATGAAATCACTGAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 1235  
Qy 481 GTTTTGAATGCTATTTTGAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 540  
Db 1236 GTTTTGAATGCTATTTTGAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 1295  
Qy 541 AATGACATTCGAAAACCTGAACTTGAATCAGGAATTCAGCTGCATGAAAGTTGCAAA 600  
Db 1296 AATGACATTCGAAAACCTGAACTTGAATCAGGAATTCAGCTGCATGAAAGTTGCAAA 1355  
Qy 601 GAGGTTCGACACGCGCTGGCGCCGCTGTAGTTGCAAAATGAGTTGCAAAAGTTGCAAC 660  
Db 1356 GAGGTTCGACACGCGCTGGCGCCGCTGTAGTTGCAAAATGAGTTGCAAAAGTTGCAAC 1415  
Qy 661 AGTATTTTGAAGAAAAGATTTTATGAAAAGATTTTAAATAATTTCTGGAAGTTAG 720  
Db 1416 AGTATTTTGAAGAAAAGATTTTATGAAAAGATTTTAAATAATTTCTGGAAGTTAG 1475  
Qy 721 TATTTTGAAGAAAAGATTTTATGAAAAGATTTTCTGATTTCC 769  
Db 1476 TATTTTGAAGAAAAGATTTTATGAAAAGATTTTCTGATTTCC 1524

RESULT 4  
ID AAF56295 standard; DNA; 158 BP.  
XX AAF56295;  
AC AAF56295;  
XX 18-APR-2001 (first entry)  
XX IS2 element sequence #2.  
DE IS2 element sequence #2.  
XX Miniature inverted repeat transposable element; MITE; duplication;  
XX regulate; IS2; ds.  
XX  
OS Daucus carota.  
XX  
XX WO200105986-A2.  
XX 25-JAN-2001.  
PD 19-JUL-2000; 2000WO-JP004837.  
XX 21-JUL-1999; 99JP-00206316.  
XX 21-JUL-1999; 99JP-00206320.  
PR 12-JUN-2000; 2000JP-00175825.  
XX (SAME-) SAN-EI GEN FFI INC.

PA (OZEK/) OZEKI Y.  
XX  
PI Ozekei Y, Oyanagi M, Fukuda T, Koda T;  
XX  
DR WPI; 2001-147351/15.  
XX  
XX Novel miniature inverted-repeat transposable element (MITE)-like element  
PT useful for constructing transgene expression cassette for stably creating  
PT genetically engineered organisms capable of expression of transgene.  
XX  
PS Disclosure; Page 103; 104pp; English.  
XX  
CC The present invention relates to a miniature inverted-repeat transposable  
CC element (MITE)-like element capable of causing duplication of a target  
CC sequence at the site of its insertion in a genomic gene. The invention is  
CC useful for causing expression of a transgene in a plant. It can also be  
CC used for inducing or regulating the expression in a plant of the gene  
CC introduced.  
XX  
SQ Sequence 158 BP; 58 A; 16 C; 35 G; 49 T; 0 U; 0 Other;  
Query Match 20.5%; Score 158; DB 4; Length 158;  
Best Local Similarity 100.0%; Pred. No. 7.2e-61;  
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 612 ACGGCTGCGCGCGCGCTGAGTTCGCAATGAGTTCGCAAAAGTTCGCAACACTATTTTGA 671  
DB 1 ACGGCTGCGCGCGCGCTGAGTTCGCAATGAGTTCGCAAAAGTTCGCAACACTATTTTGA 60  
QY 672 AAAAAAGATTATTAAGGATATTTTAAAAATATTCGAAAGTATTTTGA 731  
DB 61 AAAAAAGATTATTAAGGATATTTTAAAAATATTCGAAAGTATTTTGA 120  
QY 732 ACATTAAGAAAGGATGAGTTCGAGATTTCC 769  
DB 121 ACATTAAGAAAGGATGAGTTCGAGATTTCC 158  
RESULT 5  
AAF56294  
ID AAF56294 standard; DNA; 158 BP.  
AC AAF56294;  
XX  
DT 18-APR-2001 (first entry)  
XX  
DE IS2 element sequence #1.  
XX  
KM Miniature inverted repeat transposable element; MITE; duplication;  
KM regulate; IS2; ds.  
XX  
OS Daucus carota.  
XX  
PN WO200105986-A2.  
XX  
PD 25-JAN-2001.  
XX  
PF 19-JUL-2000; 2000WO-JP004837.  
XX  
PR 21-JUL-1999; 99JP-00206316.  
PR 21-JUL-1999; 99JP-00206320.  
PR 12-JUN-2000; 2000JP-00175825.  
XX  
PA (SANE-) SAN-EI GEN FFI INC.  
PA (OZEK/) OZEKI Y.  
XX  
PI Ozekei Y, Oyanagi M, Fukuda T, Koda T;  
XX  
DR WPI; 2001-147351/15.  
XX  
XX Novel miniature inverted-repeat transposable element (MITE)-like element  
PT useful for constructing transgene expression cassette for stably creating  
PT genetically engineered organisms capable of expression of transgene.

XX  
PS Disclosure; Page 102; 104pp; English.  
XX  
CC The present invention relates to a miniature inverted-repeat transposable  
CC element (MITE)-like element capable of causing duplication of a target  
CC sequence at the site of its insertion in a genomic gene. The invention is  
CC useful for causing expression of a transgene in a plant. It can also be  
CC used for inducing or regulating the expression in a plant of the gene  
CC introduced.  
XX  
SQ Sequence 158 BP; 47 A; 29 C; 17 G; 65 T; 0 U; 0 Other;  
Query Match 20.5%; Score 158; DB 4; Length 158;  
Best Local Similarity 100.0%; Pred. No. 7.2e-61;  
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGAATCTTTTAAAAATACCATCTGTAATATTTTAAAAATACATGCACTTT 60  
DB 1 GGAATCTTTTAAAAATACCATCTGTAATATTTTAAAAATACATGCACTTT 60  
QY 61 TCAATGTTTTTAAAAATACCTTTTCAATATTTTAAAAATACATGCACTTT 120  
DB 61 TCAATGTTTTTAAAAATACCTTTTCAATATTTTAAAAATACATGCACTTT 120  
QY 121 TTGCAACCTCATTTGCAACCTTGCGCGCGCGCGCT 158  
DB 121 TTGCAACCTCATTTGCAACCTTGCGCGCGCGCGCT 158  
RESULT 6  
AAF56291/c  
ID AAF56291 standard; DNA; 769 BP.  
AC AAF56291;  
XX  
DT 18-APR-2001 (first entry)  
XX  
DE MITE-like element 5' terminal inverted repeat sequence.  
XX  
KM Miniature inverted repeat transposable element; MITE; duplication;  
KM regulate; ds.  
XX  
OS Daucus carota.  
XX  
PN WO200105986-A2.  
XX  
PD 25-JAN-2001.  
XX  
PF 19-JUL-2000; 2000WO-JP004837.  
XX  
PR 21-JUL-1999; 99JP-00206316.  
PR 21-JUL-1999; 99JP-00206320.  
PR 12-JUN-2000; 2000JP-00175825.  
XX  
PA (SANE-) SAN-EI GEN FFI INC.  
PA (OZEK/) OZEKI Y.  
XX  
PI Ozekei Y, Oyanagi M, Fukuda T, Koda T;  
XX  
DR WPI; 2001-147351/15.  
XX  
XX Novel miniature inverted-repeat transposable element (MITE)-like element  
PT useful for constructing transgene expression cassette for stably creating  
PT genetically engineered organisms capable of expression of transgene.  
XX  
PS Claim 4; Page 98-99; 104pp; English.  
XX  
CC The present invention relates to a miniature inverted-repeat transposable  
CC element (MITE)-like element capable of causing duplication of a target  
CC sequence at the site of its insertion in a genomic gene. The invention is  
CC useful for causing expression of a transgene in a plant. It can also be  
CC used for inducing or regulating the expression in a plant of the gene  
CC introduced.

XX Sequence 769 BP; 277 A; 113 C; 141 G; 238 T; 0 U; 0 Other;

Query Match 14.6%; Score 112; DB 4; Length 769;  
Best Local Similarity 100.0%; Pred. No. 3e-40;  
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 TCCGATTTCAAGTTCAGTTTCGATGTCATTTTCGAAATCGAATATATATATAT 522  
DB 574 TCCGATTTCAAGTTCAGTTTCGATGTCATTTTCGAAATCGAATATATATATAT 515  
QY 523 ATATATATCGATTTTCGAAATGACATTCGAAACTGGAATTGAAATCAGGA 574  
DB 514 ATATATATCGATTTTCGAAATGACATTCGAAACTGGAATTGAAATCAGGA 463

RESULT 7  
AAFS6293/c  
ID AAFS6293 standard; DNA; 1192 BP.

XX AAFS6293;

AC AAFS6293;

DT 18-APR-2001 (first entry)

DE MITE-like element.

KM Miniature inverted repeat transposable element; MITE; duplication;

XX regulator; ds.

OS Daucus carota.

XX WO200105986-A2.

PD 25-JAN-2001.

PF 19-JUL-2000; 2000MO-JP004837.

PR 21-JUL-1999; 99JP-00206316.

PR 21-JUL-1999; 99JP-00206320.

PR 12-JUN-2000; 2000JP-00175825.

XX (SANE-) SAN-EI GEN FFI INC.

PA (OZEK/) OZEKI Y.

PI Ozeki Y, Oyanagi M, Fukuda T, Koda T;

XX WPI; 2001-147351/15.

DR Novel miniature inverted-repeat transposable element (MITE)-like element

PT useful for constructing transgene expression cassette for stably creating

PT genetically engineered organisms capable of expression of transgene.

PS Claim 4; Page 99-100; 104pp; English.

XX The present invention relates to a miniature inverted-repeat transposable

CC element (MITE)-like element capable of causing duplication of a target

CC sequence at the site of its insertion in a genomic gene. The invention is

CC useful for causing expression of a transgene in a plant. It can also be

CC used for inducing or regulating the expression in a plant of the gene

CC introduced

DB 912 ATATATATCGATTTTCGAAATGACATTCGAAACTGGAATTGAAATCAGGA 861

RESULT 8  
AAFS6298/c  
ID AAFS6298 standard; DNA; 1543 BP.

XX AAFS6298;

AC AAFS6298;

DT 18-APR-2001 (first entry)

DE IS2 element sequence #5.

KM Miniature inverted repeat transposable element; MITE; duplication;

XX regulator; IS2; ds.

OS Daucus carota.

XX WO200105986-A2.

PD 25-JAN-2001.

PF 19-JUL-2000; 2000MO-JP004837.

PR 21-JUL-1999; 99JP-00206316.

PR 21-JUL-1999; 99JP-00206320.

PR 12-JUN-2000; 2000JP-00175825.

XX (SANE-) SAN-EI GEN FFI INC.

PA (OZEK/) OZEKI Y.

PI Ozeki Y, Oyanagi M, Fukuda T, Koda T;

XX WPI; 2001-147351/15.

DR Novel miniature inverted-repeat transposable element (MITE)-like element

PT useful for constructing transgene expression cassette for stably creating

PT genetically engineered organisms capable of expression of transgene.

PS Disclosure; Page 103-104; 104pp; English.

XX The present invention relates to a miniature inverted-repeat transposable

CC element (MITE)-like element capable of causing duplication of a target

CC sequence at the site of its insertion in a genomic gene. The invention is

CC useful for causing expression of a transgene in a plant. It can also be

CC used for inducing or regulating the expression in a plant of the gene

CC introduced

XX Sequence 1543 BP; 569 A; 244 C; 214 G; 516 T; 0 U; 0 Other;

Query Match 14.6%; Score 112; DB 4; Length 1543;  
Best Local Similarity 100.0%; Pred. No. 3e-40;  
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 TCCGATTTCAAGTTCAGTTTCGATGTCATTTTCGAAATCGAATATATATATAT 522  
DB 1322 TCCGATTTCAAGTTCAGTTTCGATGTCATTTTCGAAATCGAATATATATATAT 1270  
QY 523 ATATATATCGATTTTCGAAATGACATTCGAAACTGGAATTGAAATCAGGA 574  
DB 1269 ATATATATCGATTTTCGAAATGACATTCGAAACTGGAATTGAAATCAGGA 1218

RESULT 9  
AAFS6294/c  
ID AAFS6294 standard; DNA; 158 BP.

XX AAFS6294;

AC AAFS6294;

DT 18-APR-2001 (first entry)

DE IS2 element sequence #1.



KW Miniature inverted repeat transposable element; MITE; duplication;  
KM regulate; IS2; ds.  
XX Daucus carota.  
XX OS  
XX WO200105986-A2.  
XX PN  
XX 25-JAN-2001.  
XX PD  
XX 19-JUL-2000; 2000WO-JP004837.  
XX PF  
XX 21-JUL-1999; 99JP-00206316.  
XX PR 21-JUL-1999; 99JP-00206320.  
XX PR 12-JUN-2000; 2000JP-00175825.  
XX PA (SANE-) SAN-EI GEN FFI INC.  
XX (OZEK/) OZEKI Y.  
XX PI Ozeki Y, Oyanagi M, Fukuda T, Koda T;  
XX WPI; 2001-147351/15.  
XX DR  
XX Novel miniature inverted-repeat transposable element (MITE)-like element  
PT useful for constructing transgene expression cassette for stably creating  
PT genetically engineered organisms capable of expression of transgene.  
XX PS Disclosure; Page 102; 104pp; English.  
XX XX  
XX The present invention relates to a miniature inverted-repeat transposable  
CC element (MITE)-like element capable of causing duplication of a target  
CC sequence at the site of its insertion in a genomic gene. The invention is  
CC useful for causing expression of a transgene in a plant. It can also be  
CC used for inducing or regulating the expression in a plant of the gene  
CC introduced  
XX CC  
SQ Sequence 158 BP; 47 A; 29 C; 17 G; 65 T; 0 U; 0 Other;  
Query Match 3.9%; Score 30; DB 4; Length 158;  
Best Local Similarity 100.0%; Pred. No. 0.0019;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 205 GTTGC AATGAGTGC AATGTC AAT 234  
DB 140 GTTGC AATGAGTGC AATGTC AAT 111  
RESULT 10  
AAF56295/C  
ID AAF56295 standard; DNA; 158 BP.  
XX  
XX AAF56295;  
XX AC  
XX 18-APR-2001 (first entry)  
XX DT  
XX IS2 element sequence #2.  
XX DE  
XX Miniature inverted repeat transposable element; MITE; duplication;  
KM regulate; IS2; ds.  
XX KW  
XX Daucus carota.  
XX OS  
XX WO200105986-A2.  
XX PN  
XX 25-JAN-2001.  
XX PD  
XX 19-JUL-2000; 2000WO-JP004837.  
XX PF  
XX 21-JUL-1999; 99JP-00206316.  
XX PR 21-JUL-1999; 99JP-00206320.  
XX PR 12-JUN-2000; 2000JP-00175825.  
XX PA (SANE-) SAN-EI GEN FFI INC.  
XX (OZEK/) OZEKI Y.  
XX PI

XX Ozeki Y, Oyanagi M, Fukuda T, Koda T;  
XX WPI; 2001-147351/15.  
XX DR  
XX Novel miniature inverted-repeat transposable element (MITE)-like element  
PT useful for constructing transgene expression cassette for stably creating  
PT genetically engineered organisms capable of expression of transgene.  
XX PS Disclosure; Page 103; 104pp; English.  
XX XX  
XX The present invention relates to a miniature inverted-repeat transposable  
CC element (MITE)-like element capable of causing duplication of a target  
CC sequence at the site of its insertion in a genomic gene. The invention is  
CC useful for causing expression of a transgene in a plant. It can also be  
CC used for inducing or regulating the expression in a plant of the gene  
CC introduced  
XX CC  
SQ Sequence 158 BP; 58 A; 16 C; 35 G; 49 T; 0 U; 0 Other;  
Query Match 3.8%; Score 29; DB 4; Length 158;  
Best Local Similarity 100.0%; Pred. No. 0.0052;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 112 TTTCG AACTTTTCG AACTTCATTTGCAAC 140  
DB 48 TTTCG AACTTTTCG AACTTCATTTGCAAC 20  
RESULT 11  
ABE21958  
ID ABE21958 standard; DNA; 2717 BP.  
XX  
XX ABE21958;  
XX AC  
XX 26-MAR-2002 (first entry)  
XX DT  
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 17347.  
XX DE  
XX Drosophila; developmental biology; cell signalling; insecticide;  
XX KM pharmaceutical; gene; ds.  
XX KW  
XX Drosophila melanogaster.  
XX OS  
XX WO200171042-A2.  
XX PN  
XX 27-SEP-2001.  
XX PD  
XX 23-MAR-2001; 2001WO-US009231.  
XX PF  
XX 23-MAR-2000; 2000US-0191637P.  
XX PR 11-JUL-2000; 2000US-00614150.  
XX PR  
XX (PEKE ) PS CORP NY.  
XX PA  
XX Venter JC, Adams M, Li PWD, Myers EM;  
XX WPI; 2001-656860/75.  
XX DR  
XX New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signalling and cell-cell  
PT interactions.  
XX PT  
XX Claim 1; SEQ ID NO 17347; 21pp + Sequence Listing; English.  
XX PS  
XX The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABE16176-ABE30511), expressed DNA  
CC sequences (ABE1840-ABE16175) and the encoded proteins (ABE57737-  
CC ABE72072). The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly  
 CC from WIFO at ftp.wifo.int/pub/published\_pct\_sequences

XX Sequence 2717 BP, 835 A; 555 C; 503 G; 824 T; 0 U; 0 Other;

Query Match 3.8%; Score 29; DB 4; Length 2717;  
 Best Local Similarity 100.0%; Pred. No. 0.0051;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 501 AATCGATATATATATATATATATATATATA 529  
 DB 767 AATCGATATATATATATATATATATATA 795

# RESULT 12

ABL21958/C  
 ID ABL21958 standard; DNA; 2717 BP.

XX ABL21958;

DT 26-MAR-2002 (first entry)

XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 17347.  
 XX Drosophila; developmental biology; cell signalling; insecticide;  
 XX pharmaceutical; gene; ds.  
 XX Drosophila melanogaster.

PN WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US009231.

PR 23-MAR-2000; 2000US-0191637P.

PR 11-JUL-2000; 2000US-00614150.

XX (PEKE ) PE CORP NY.

PI Venter JC, Adams M, Li PMD, Myers EW;

DR WPI; 2001-656860/75.

XX New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signaling and cell-cell  
 PT interactions.

XX Claim 1; SEQ ID NO 17347; 21bp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signaling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABU16176-ABU30511), expressed DNA  
 CC sequences (ABU1840-ABU16175) and the encoded proteins (ABBS7737-  
 CC ABBS7072). The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIFO at ftp.wifo.int/pub/published\_pct\_sequences

XX Sequence 2717 BP, 835 A; 555 C; 503 G; 824 T; 0 U; 0 Other;

Query Match 3.8%; Score 29; DB 4; Length 2717;  
 Best Local Similarity 100.0%; Pred. No. 0.0051;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 508 TATATATATATATATATATATATCGATT 536  
 DB 795 TATATATATATATATATATATATCGATT 767

# RESULT 13

ABN81058  
 ID ABN81058 standard; DNA; 466 BP.

XX ABN81058;

DT 16-JUL-2002 (first entry)

XX Shrimp polynucleotide SEQ ID NO 62.

QY Giant black tiger prawn; Penaeus monodon; pacific white shrimp;  
 KW Litopenaeus vannamei; shrimp; microsatellite sequence; genome mapping;  
 KW Taura Syndrome Virus; TSV; infection; ds.

XX Penaeus monodon.

PN WO200034476-A2.

PD 15-JUN-2000.

PF 10-DEC-1999; 99WO-US029571.

PR 10-DEC-1998; 98US-0111670P.

XX (TUFT ) TUFTS COLABSE.

PI Alciivar-Warren A, Xu Z, Dhar AK, Fan Y, Meenan D, Garcia DK;

DR WPI; 2000-423422/36.

XX Polynucleotides of shrimp are useful for identifying, mapping and  
 PT characterizing of the genome of various species of shrimp.

XX Claim 1; Page 91; 120pp; English.

XX The invention relates to an isolated polynucleotide (I) of the giant  
 CC black tiger prawn, Penaeus monodon or expressed sequence tags of the  
 CC pacific white shrimp, Litopenaeus vannamei (ABN80997-ABN81172), both  
 CC containing microsatellites sequences including those P. monodon  
 CC microsatellite sequences given in GenBank AF077550-AF077558. (I), the  
 CC complementary sequence or fragment and the encoded polypeptide are useful  
 CC for mapping of the genome of various species of shrimp. Mapping the  
 CC genome of Penaeus is useful for determining whether a test shrimp,  
 CC preferably Litopenaeus vannamei, has a genotype associated with a  
 CC phenotypic trait such as resistance to Taura Syndrome Virus (TSV)  
 CC infection

XX Sequence 466 BP, 146 A; 97 C; 91 G; 132 T; 0 U; 0 Other;

Query Match 3.6%; Score 28; DB 3; Length 466;  
 Best Local Similarity 100.0%; Pred. No. 0.015;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 503 ATCGATATATATATATATATATATATATAT 530  
 DB 95 ATCGATATATATATATATATATATATATAT 122

# RESULT 14

ABN81058/C  
 ID ABN81058 standard; DNA; 466 BP.

XX ABN81058;

DT 16-JUL-2002 (first entry)

XX Shrimp polynucleotide SEQ ID NO 62.

QY Giant black tiger prawn; Penaeus monodon; pacific white shrimp;  
 KW Litopenaeus vannamei; shrimp; microsatellite sequence; genome mapping;  
 KW Taura Syndrome Virus; TSV; infection; ds.

XX Penaeus monodon.



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OM nucleic - nucleic search, using SW model

Run on: July 4, 2004, 22:15:37 ; Search time 2676 Seconds

(without alignments)  
8581.471 Million cell updates/sec

Title: US-10-031-818b-1  
Sequence score: 769  
Sequence: 1 GGGATCTTCTTAAATACC.....GGAGCTTGTGATGATTCCTCC 769

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Labeling first 45 summaries

Database :

EST:  
1: em\_escba:\*  
2: em\_escba:\*  
3: em\_escin:\*  
4: em\_escmu:\*  
5: em\_escov:\*  
6: em\_escpl:\*  
7: em\_escro:\*  
8: em\_escr:\*  
9: gb\_esc1:\*  
10: gb\_esc2:\*  
11: gb\_esc3:\*  
12: gb\_esc4:\*  
13: gb\_esc5:\*  
14: gb\_esc6:\*  
15: em\_escfun:\*  
16: em\_escfun:\*  
17: em\_escfun:\*  
18: em\_escfun:\*  
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21: em\_escfun:\*  
22: em\_escfun:\*  
23: em\_escfun:\*  
24: em\_escfun:\*  
25: em\_escfun:\*  
26: em\_escfun:\*  
27: em\_escfun:\*  
28: gb\_esc1:\*  
29: gb\_esc2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	30	3.9	186	12	BI795040 H006F09 E
2	30	3.9	186	12	BI795040 H006F09 E
3	30	3.9	297	12	BI799513 H134C11 E
4	30	3.9	297	12	BI799513 H134C11 E

5	30	3.9	345	14	CB966625 NL40_C10
6	30	3.9	345	14	CB966625 NL40_C10
7	30	3.9	348	13	BU673472 NL_15_82
8	30	3.9	348	13	BU673472 NL_15_82
9	30	3.9	358	12	BI306298 NL_4_B15
10	30	3.9	358	12	BI306298 NL_4_B15
11	30	3.9	535	12	BI305924 NL_2_H20
12	30	3.9	535	12	BI305924 NL_2_H20
13	30	3.9	577	13	BU673763 NL_19_92
14	30	3.9	577	13	BU673763 NL_19_92
15	30	3.9	633	12	BI306166 NL_3_007
16	30	3.9	633	12	BI306166 NL_3_007
17	30	3.9	638	14	CB964597 NL8_G07 D
18	30	3.9	638	14	CB964597 NL8_G07 D
19	30	3.9	644	14	CB966543 NL3_806
20	30	3.9	644	14	CB966543 NL3_806
21	30	3.9	648	14	CB617907 OSIEB01G
22	30	3.9	648	14	CB617907 OSIEB01G
23	30	3.9	772	14	CB625169 OSIEB01G
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25	29	3.8	319	28	BI184153 024_L_22-
26	29	3.8	319	28	BI184153 024_L_22-
27	29	3.8	319	29	CSN07P55 T3 end of
28	29	3.8	319	29	CSN07P55 T3 end of
29	29	3.8	473	28	BH200037 Sm1_53A2.
30	29	3.8	473	28	BH200037 Sm1_53A2.
31	29	3.8	482	28	AQ970964 RPT-23-3
32	29	3.8	482	28	AQ970964 RPT-23-3
33	29	3.8	497	28	BH200889 Sm1_41113
34	29	3.8	497	28	BH200889 Sm1_41113
35	29	3.8	586	14	CD082704 MA3_9989U
36	29	3.8	586	14	CD082704 MA3_9989U
37	29	3.8	607	28	BH543165 BOCME35TR
38	29	3.8	607	28	BH543165 BOCME35TR
39	29	3.8	733	29	BX235983 Danilo rer
40	29	3.8	733	29	BX235983 Danilo rer
41	28	3.6	210	29	CG314411 OGBOQ35TH
42	28	3.6	210	29	CG314411 OGBOQ35TH
43	28	3.6	330	28	B2198852 CH230-494
44	28	3.6	330	28	B2198852 CH230-494
45	28	3.6	333	12	BI504445 BB170002A

#### ALIGNMENTS

RESULT 1  
LOCUS BI795040  
DEFINITION H006F09 Endospore library from Oryza sativa (10 days after anthesis)  
ORIGIN Oryza sativa cDNA clone H006F09, mRNA sequence.  
ACCESSION BI795040  
VERSION BI795040.1 GI:15846764  
KEYWORDS  
SOURCE  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
AUTHORS Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X., Wu, H.F., Jiang, Y.X., Yu, F.C., Gao, Q.K. and Lou, Y.C.  
TITLE A Gene Expression Screen in Oryza sativa  
JOURNAL Unpublished (2001)  
COMMENT Contact: Haitao Dong, Dehao Li  
Bioinformatics and Gene Network Research Group  
Zhejiang University  
Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China  
Tel: 0086-571-86961525  
Fax: 0086-571-86961525  
Email: webmaster@estarray.org, URL: http://www.estarray.org  
Seq primer: M13 forward primer.  
Location/Qualifiers

#### FEATURES



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/mot_type="mRNA"
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Db	177	AAATCGATATATATATATATATATATAT	148		

RESULT 5				
CB966625				
LOCUS	CB966625			
DEFINITION	MD40_C10 Drought stress (leaf) Oryza sativa (indica cultivar-group)	345 bp	mRNA	linear EST 29-APR-2003
ACCESSION:	MD40_clone MD40_C10 3', mRNA sequence.			
VERSION	CB966625			
KEYWORDS	CB966625.1 GI:30228735			
SOURCE	EST.			
ORGANISM	Oryza sativa (indica cultivar-group)			
	Oryza sativa (indica cultivar-group)			

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (pages 1 to 345)	Markandeya, G., Ravindra Babu, P., Venkat Reddy, B., Nagabushnana, I., Chandra Sekhar, A., Bonnenzen, J. L., Ramakrishna, W. and Reddy, A.R.	ESTs from a normalized cDNA library of drought stressed rice seedlings (Oryza sativa L. cv Nagina 22)	Unpublished (2003)	Contact: Reddy AR

Department of Plant Sciences, School of Life Sciences  
University of Hyderabad  
P.O. Central University, Hyderabad-500 046, A.P., India  
Tel.: 0091-40-3010265  
Fax: 0091-40-3010145  
Email: arjuns@uohyd.ernet.in  
Insert Length: 345 Std Error: 0.00  
Seq primer: CGCCAGCGTTTCCAGTCACAC.  
Location/Qualifiers  
1..345

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Best Local Similarity 100.0%; Prod. No. 0.12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

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RESULT 6	CB966625/c	LOCUS	CB966625	345 bp	mRNA	Linear	EST 29-APR-2003

DEFINITION	NI40 C10 Drought stress (leaf) Oryza sativa (indica cultivar-group)
ACCESSION	CB966625
VERSION	CB966625.1
KEYWORDS	GI:30228735
SOURCE	EST.
ORGANISM	Oryza sativa (indica cultivar-group)
	Oryza sativa (indica cultivar-group)
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE	1 (bases 1 to 345)
AUTHORS	Markandeya,G., Ravindra Babu,P., Venkat Reddy,B., Nagabhushana,I., Chandra Sekhar,A., Bennerzen,J.L., Ramakrishna,M. and Reddy,A.R.
TITLE	ESTs from a normalized cDNA library of drought stressed rice seedlings (Oryza sativa L.cv Nagina 22)
JOURNAL	Unpublished (2003)
COMMENT	Contact: Reddy AR Department of Plant Sciences, School of Life Sciences University of Hyderabad P.O. Central University, Hyderabad-500 046, A.P., India Tel: 0091-40-3010265 Fax: 0091-40-3010145 Email: arjulsleu@uhyd.ernet.in Insert length: 345 Std Error: 0.00 Seq primer: GCGACGGTTTCCACATCAACAC.
FEATURES	Location/Qualifiers
SOURCE	1..345

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Query March          3.3%; Score 30; DB 14; Length 345;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db       135 AATATATATATATATATATTCGATTT 106

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RESULT 7	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT			
BU673472	BU673472	BU673472	BU673472	BU673472	BU673472.1	GI:23514110	EST.	Oryza sativa (indica cultivar-group)	Oryza sativa (indica cultivar-group)	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.	1 (bases 1 to 348)	Reddy,A.R., Markandeya,G., Ramakrishna,M., Nagabhushana,I., Ravindra Babu,P., Madana Mohan Reddy,A., Chandra Sekhar,A. and Bannetzer,J.L.	Novel EST enrichment with normalized cDNA libraries from drought stressed rice (Oryza sativa L.cv Nagina 22) (2002)	Unpublished (2002)	Contact: Reddy AR

University of Hyderabad  
P.O. Central University, Hyderabad-500 046, A.P., India  
Tel.: 0091-40-3010265



Fax: 0091-40-3010145  
Email: arjulis@uohyd.ernet.in  
Insert length: 348 Std Error: 0.00  
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# FEATURES

Location/Qualifiers

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/clone="NL\_15\_82"  
/tissue\_type="Embryonic leaf tissue"  
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# ORIGIN

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Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 501 AATCGATATATATATATATATATATAT 530  
109 AATCGATATATATATATATATATATAT 138

RESULT 8 BUE73472 348 bp mRNA linear EST 07-OCT-2002  
LOCUS BUE73472/c NL\_15\_82 Drought stress (leaf) Oryza sativa (indica cultivar-group)  
DEFINITION BUE73472 cDNA clone NL\_15\_82 3', mRNA sequence.  
ACCESSION BUE73472.1 GI:23514110  
VERSION BUE73472.1  
KEYWORDS EST.  
SOURCE Oryza sativa (indica cultivar-group)  
ORGANISM Oryza sativa (indica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 348)  
Reddy,A.R., Marandeya,G., Ramakrishna,W., Nagabhushana,I., Ravindra Babu,P., Madana Mohan Reddy,A., Chandra Sekhar,A. and Bennezen,J.L.  
Novel EST enrichment with normalized cDNA libraries from drought stressed rice (Oryza sativa L.cv Nagina 22) (2002)  
Unpublished (2002)  
Contact: Reddy AR  
Department of Plant Sciences, School of Life Sciences  
University of Hyderabad  
P.O. Central University, Hyderabad-500 046, A.P, India  
Tel: 0091-40-3010265  
Fax: 0091-40-3010145  
Email: arjulis@uohyd.ernet.in  
Insert length: 348 Std Error: 0.00  
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# FEATURES

Location/Qualifiers

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OY 501 AATCGATATATATATATATATATATAT 530  
109 AATCGATATATATATATATATATATAT 138

RESULT 10 B1306298/c 358 bp mRNA linear EST 20-JUL-2001  
LOCUS B1306298 NL\_4\_B15 Drought stress (leaf) Oryza sativa (indica cultivar-group)  
DEFINITION B1306298 cDNA clone NL\_4\_B15 3', mRNA sequence.  
ACCESSION B1306298.1 GI:14981620  
VERSION B1306298.1  
KEYWORDS EST.  
SOURCE Oryza sativa (indica cultivar-group)  
ORGANISM Oryza sativa (indica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

# ORIGIN

Query Match 3.9%; Score 30; DB 13; Length 348;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 507 ATATATATATATATATATATATATATATAT 536  
138 ATATATATATATATATATATATATATATAT 109

RESULT 9 B1306298 358 bp mRNA linear EST 20-JUL-2001  
LOCUS B1306298 NL\_4\_B15 Drought stress (leaf) Oryza sativa (indica cultivar-group)  
DEFINITION B1306298 cDNA clone NL\_4\_B15 3', mRNA sequence.  
ACCESSION B1306298.1 GI:14981620  
VERSION B1306298.1  
KEYWORDS EST.  
SOURCE Oryza sativa (indica cultivar-group)  
ORGANISM Oryza sativa (indica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

# REFERENCE

1 (bases 1 to 358)  
Reddy,A.R., Ramakrishna,W., Chandrasekhar,A., Nagabhushan,I., Ravindrababu,P. and Bennezen,J.L.  
Novel EST enrichment with normalized cDNA libraries from drought stressed rice (Oryza sativa L.cv Nagina 22)  
Unpublished (2001)  
Contact: Reddy AR  
Department of Plant Sciences, School of Life Sciences  
University of Hyderabad  
P.O. Central University, Hyderabad-500 046, A.P, India  
Tel: 0091-40-3010265  
Fax: 0091-40-3010145  
Email: arjulis@uohyd.ernet.in  
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# FEATURES

Location/Qualifiers

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Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 501 AATCGATATATATATATATATATATAT 530  
109 AATCGATATATATATATATATATATAT 138

RESULT 10 B1306298/c 358 bp mRNA linear EST 20-JUL-2001  
LOCUS B1306298 NL\_4\_B15 Drought stress (leaf) Oryza sativa (indica cultivar-group)  
DEFINITION B1306298 cDNA clone NL\_4\_B15 3', mRNA sequence.  
ACCESSION B1306298.1 GI:14981620  
VERSION B1306298.1  
KEYWORDS EST.  
SOURCE Oryza sativa (indica cultivar-group)  
ORGANISM Oryza sativa (indica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

# ORIGIN

Query Match 3.9%; Score 30; DB 12; Length 358;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TITLE  
Ravindrababu, P. and Bennetzen, J.L.  
Novel EST enrichment with normalised cDNA libraries from drought  
stressed rice (Oryza sativa L. cv Nagina 22)  
JOURNAL  
Unpublished (2001)  
COMMENT  
Contact: Kedy AR

Department of Plant Sciences, School of Life Sciences  
University of Hyderabad  
P.O. Central University, Hyderabad-500 046, A.P., India  
Tel.: 0091-40-3010265  
Fax: 0091-40-3010145  
Email: arjuls@uohyd.ernet.in.  
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Location/Qualifiers

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Db	138	ATATATATATATATATATATATGATT	109	

RESULT 11	LOCUS	DEFINITION	ACCSSION#	VERSION	KEYWORDS	SOURCE
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		535 bp mRNA linear EST 20-JUL-2001				
		cdna-clone NL_2_H2O 3', mRNA sequence.				
			B1305924.1	GI:14581246		

REFERENCE	1 (bases 1 to 535)
AUTHORS	Reddy A.R., Ramakrishna, M., Chandrasekhar, A., Nagabhushan, I., Ravindrababu, P. and Bennezeen, J.L.
TITLE	Novel EST enrichment with normalised cDNA libraries from drought stressed rice ( <i>Oryza sativa</i> L. cv Nagina 22)
JOURNAL	Unpublished (2001)
COMMENT	Contact: Reddy AR

JOURNAL  
 COMMENT  
 Unpublished (2001)  
 Contact: Reddy AR  
 Department of Plant Sciences, School of Life Sciences  
 University of Hyderabad  
 P.O. Central University, Hyderabad-500 046, A.P, India  
 Tel.: 0091-40-3010265  
 Fax: 0091-40-3010145  
 Email: arjuls@uoyd.ernet.in  
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Db	ATATATATATATATATATATATATCGAATTT	418		

RESULT	12
BI305924/c	
LOCUS	BI305924
DEFINITION	Mt_2_H2O Drought stresses (leaf) Oryza sativa (indica cultivar-group)
ACCESSION	BI305924
VERSION	BI305924.1
KEYWORDS	GI:14981246
SOURCE	EST.
ORGANISM	Oryza sativa (indica cultivar-group)
	Oryza sativa (indica cultivar-group)

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 535)	Reddy A.R., Ramakrishna, W., Chandrasekhar, A., Nagabushan, I., Ravindrababu, P. and Benerjee, J. L.	Novel EST enrichment with normalized cDNA libraries from drought stressed rice ( <i>Oryza sativa</i> L. cv Nagina 22)	Unpublished (2001)	Contact: Reddy AR

Department of Plant Sciences, School of Life Sciences  
University of Hyderabad  
P.O. Central University, Hyderabad-500 046, A.P., India  
Tel.: 0091-40-310265  
Fax: 0091-40-310145  
Email: arjun@uhyd.ernet.in  
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Location/Qualifiers  
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Db       418 AATCGATATATATATATATATATATAT 389

RESULT 13
LOCUS      BUS73763
DEFINITION BUS73763 577 bp mRNA linear EST_07-OCT-2007
            NL_19_92 Drought stress [leaf] Oryza sativa (indica cultivar-group)
            cDNA clone NL_19_92 3', mRNA sequence.

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VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	ORIGIN	Db	cy
BUE73763	GI:23514684	EST	Oryza sativa (indica cultivar-group)	Oryza sativa (indica cultivar-group)	Reddy A.R., Markandeya, G., Ramakrishna, W., Nagabhushana, I., Ravindra Babu, P., Madana Mohan Reddy, A., Chandra Sekhar, A. and Benneetzen, J.L.	Novel EST enrichment with normalized cDNA libraries from drought stressed rice (Oryza sativa L. cv Nagina 22) (2002)	Unpublished (2002)	Contact: Reddy AR Department of Plant Sciences, School of Life Sciences University of Hyderabad P.O. Central University, Hyderabad-500 046, A.P, India Tel: 0091-40-3010265 Fax: 0091-40-3010145	Location/Qualifiers 1..577 /organism="Oryza sativa (indica cultivar-group)" /mol_type="mRNA" /cultivar="Nagina 22 (indica sub sp)" /db_xref="taxon:39946" /clone="NL_19_92" /tissue_type="Embryonic leaf tissue" /dev_stage="35 day-old seedlings" /clone_lib="Drought stress (leaf)" /note="Organ: Leaf; Vector: T773Pac; ESTs from normalized leaf cDNA library from drought stressed seedlings"	Query Match 3.9%; Score 30; DB 13; Length 577; Best Local Similarity 100.0%; Pred. No. 0.901; Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	391	507
RESULT 14	BUE73763/c	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
BUE73763	577 bp	mRNA	linear	EST 07-OCT-2002			Oryza sativa (indica cultivar-group)	Oryza sativa (indica cultivar-group)	Reddy A.R., Markandeya, G., Ramakrishna, W., Nagabhushana, I., Ravindra Babu, P., Madana Mohan Reddy, A., Chandra Sekhar, A. and Benneetzen, J.L.	Novel EST enrichment with normalized cDNA libraries from drought stressed rice (Oryza sativa L. cv Nagina 22) (2002)	Unpublished (2002)	Contact: Reddy AR Department of Plant Sciences, School of Life Sciences University of Hyderabad P.O. Central University, Hyderabad-500 046, A.P, India Tel: 0091-40-3010265 Fax: 0091-40-3010145

Email: arjulsleuohyd.ernet.in  
 Insert Length: 577 Std Error: 0.00  
 Seq primer: CGCAGGATTTCCGACGACGAC.  
 Location/Qualifiers  
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ORIGIN  
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Oy 501 AAATGATATATATATATATATATATATATAT 530  
 420 AAATGATATATATATATATATATATATATAT 391

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 BI306166.1 GI:14981488  
 EST.  
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 Oryza sativa (indica cultivar-group)  
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 Ehrhartoideae; Oryzeae; Oryza.  
 1 (bases 1 to 633)  
 Reddy,A.R., Ramakrishna,W., Chandrasekhar,A., Nagabushan,I.,  
 Ravindrababu,P. and Benmetzen,J.L.  
 Novel EST enrichment with normalized cDNA libraries from drought  
 stressed rice (Oryza sativa L.cv Nagina 22)  
 Unpublished (2001)

JOURNAL  
 COMMENT  
 Contact: Reddy AR  
 Department of Plant Sciences, School of Life Sciences  
 University of Hyderabad  
 P.O. Central University, Hyderabad-500 046, A.P, India  
 Tel: 0091-40-3010265  
 Fax: 0091-40-3010145  
 Email: arjulsleuohyd.ernet.in  
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 /issue\_type="Entire leaf tissue"  
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 /note="Organ: Leaf; Vector: VT3Pac; ESTs from normalized leaf cDNA library from drought stressed seedlings"

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Tue Jul 6 09:07:34 2004

us-10-031-818b-1.011.rst

Page 7

Qy 501 AAATCGATATATATATATATATATATAT 530  
DB 109 AAATCGATATATATATATATATATATAT 138

Search completed: July 5, 2004, 00:57:37  
Job time : 2679 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OK nucleic - nucleic search, using sw model

Run on: July 4, 2004, 22:00:21 ; Search time 82 Seconds

(without alignments)  
5204.357 Million cell updates/sec

Title: US-10-031-818b-1

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Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

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Maximum DB seq length: 2000000000

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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RESULT 1  
US-08-984-320-2  
Sequence 2, Application US/08984320  
Patent No. 6222097  
GENERAL INFORMATION:  
APPLICANT: Mcbride, Kevin B.  
APPLICANT: Stalker, David M.  
TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESS: Calgene, Inc.  
STREET: 1920 Fifth Street  
CITY: Davis  
STATE: CA  
COUNTRY: USA  
ZIP: 95616  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 7.1  
SOFTWARE: Microsoft Word 5.1 (a)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/984,320  
FILING DATE:  
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APPLICATION NUMBER: US/08/487,087  
FILING DATE: 07-JUN-95  
APPLICATION NUMBER: USSN 07/998,158  
FILING DATE: 29-DEC-92  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 07/554,195  
FILING DATE: 17-JUL-90  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 07/382,518  
FILING DATE: 19-JUL-89  
ATTORNEY/AGENT INFORMATION:  
NAME: Donna E. Scherer  
REGISTRATION NUMBER: 34,719  
NAME: Carl J. Schmedler  
REGISTRATION NUMBER: 36,924  
TELEPHONE/DOCKET NUMBER: CGNE 91-1  
TELEPHONE: (916) 753-6313  
TELEFAX: (916) 753-1510  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3528 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double

Page 2

507 ATATATATATATATATATATCGA 533

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GENERAL INFORMATION:
APPLICANT: McBride, Kevin E.
APPLICANT: Stalder, David M.
TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors
NUMBER OF SEQUENCES: 6

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;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Calgene, Inc.  
;; STREET: 1920 Fifth Street  
;; CITY: Davis  
;; STATE: CA  
;; COUNTRY: USA  
;; ZIP: 95616  
;;  
;; COMPUTER READABLE FORM:  
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;; APPLICATION NUMBER: USSN 07/382,518  
;; FILING DATE: 19-JUL-89  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Donna E. Scherer  
;; REGISTRATION NUMBER: 34,719  
;; NAME: Carl J. Schwedler  
;; REGISTRATION NUMBER: 36,924  
;; REFERENCE/DOCKET NUMBER: CGNE 91-1  
;; TELECOMMUNICATION INFORMATION:  
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DB 2413 ATATATATATATATATATATCGA 2387  
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;; Sequence 2, Application US/08397653B  
;; Patent No. 6329570  
;; GENERAL INFORMATION:  
;; APPLICANT: Martineau, Belinda  
;; TITLE OF INVENTION: COTTON MODIFICATION USING  
;; TITLE OF INVENTION: OVARY-TISSUE TRANSCRIPTIONAL  
;; TITLE OF INVENTION: FACTORS  
;; NUMBER OF SEQUENCES: 10  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Calgene, Inc.  
;; STREET: 1920 Fifth Street  
;; CITY: Davis  
;; STATE: CA  
;; COUNTRY: USA  
;; ZIP: 95616  
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;; FILING DATE: 28-FEB-1995  
;; CLASSIFICATION: 800  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Elizabeth Lassen  
;; REGISTRATION NUMBER: 31,845  
;; NAME: Donna E. Scherer  
;; REGISTRATION NUMBER: 34,719  
;; NAME: Carl J. Schwedler  
;; REGISTRATION NUMBER: 36,924  
;; REFERENCE/DOCKET NUMBER: CGNE 112  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (916) 753-6313  
;; TELEFAX: (916) 753-1510  
;; INFORMATION FOR SEQ ID NO: 2:  
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;; TYPE: nucleic acid  
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;; TOPOLOGY: linear  
;; MOLECULE TYPE: cDNA to mRNA  
;; US-08-397-653B-2  
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RESULT 6  
US-08-397-653B-2/c  
;; Sequence 2, Application US/08397653B  
;; Patent No. 6329570  
;; GENERAL INFORMATION:  
;; APPLICANT: Martineau, Belinda  
;; TITLE OF INVENTION: COTTON MODIFICATION USING  
;; TITLE OF INVENTION: OVARY-TISSUE TRANSCRIPTIONAL  
;; TITLE OF INVENTION: FACTORS  
;; NUMBER OF SEQUENCES: 10  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Calgene, Inc.  
;; STREET: 1920 Fifth Street  
;; CITY: Davis  
;; STATE: CA  
;; COUNTRY: USA  
;; ZIP: 95616  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB  
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;; SOFTWARE: Microsoft Word 5.1a  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/397,653B  
;; FILING DATE: 28-FEB-1995  
;; CLASSIFICATION: 800  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Elizabeth Lassen  
;; REGISTRATION NUMBER: 31,845  
;; NAME: Donna E. Scherer  
;; REGISTRATION NUMBER: 34,719  
;; NAME: Carl J. Schwedler  
;; REGISTRATION NUMBER: 36,924  
;; REFERENCE/DOCKET NUMBER: CGNE 112  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (916) 753-6313  
;; TELEFAX: (916) 753-1510  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:

LENGTH: 4383 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
US-08-397-653B-2

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; Patent No. 5175095  
; APPLICANT: Martineau, Belinda M., Houck, Catherine M.  
; TITLE OF INVENTION: OVARY TISSUE TRANSCRIPTIONAL FACTORS  
; NUMBER OF SEQUENCES: 9  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/554,195  
; FILING DATE: 17-JUL-1990  
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DB 2387 TCGATATATATATATATATATATAT 2413

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; APPLICANT: Martineau, Belinda M., Houck, Catherine M.  
; TITLE OF INVENTION: OVARY TISSUE TRANSCRIPTIONAL FACTORS  
; NUMBER OF SEQUENCES: 9  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/554,195  
; FILING DATE: 17-JUL-1990  
; SEQ ID NO: 4:  
; LENGTH: 4383

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QY 507 ATATATATATATATATATATATCGA 533  
DB 2413 ATATATATATATATATATATATCGA 2387

RESULT 9  
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; Patent No. 5177307  
; APPLICANT: HOUCK, CATHERINE M., PEAR, JULIE R., MARTINEAU,  
; BELINDA M., HIATT, WILLIAM  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  
; MODULATIONS OF ENDOGENOUS CYTOKININ LEVELS  
; NUMBER OF SEQUENCES: 6  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/554,196  
; FILING DATE: 17-JUL-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 382,802

; FILING DATE: 19-JUL-1989  
; APPLICATION NUMBER: 188,361  
; FILING DATE: 29-APR-1988  
; APPLICATION NUMBER: 168,190  
; FILING DATE: 15-MAR-1988  
; APPLICATION NUMBER: 54,369  
; FILING DATE: 26-MAY-1987  
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5177307-1

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QY 504 TCGATATATATATATATATATATAT 530  
DB 2387 TCGATATATATATATATATATATAT 2413

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; Patent No. 5177307  
; APPLICANT: HOUCK, CATHERINE M., PEAR, JULIE R., MARTINEAU,  
; BELINDA M., HIATT, WILLIAM  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  
; MODULATIONS OF ENDOGENOUS CYTOKININ LEVELS  
; NUMBER OF SEQUENCES: 6  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/554,196  
; FILING DATE: 17-JUL-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 382,802  
; FILING DATE: 19-JUL-1989  
; APPLICATION NUMBER: 188,361  
; FILING DATE: 29-APR-1988  
; APPLICATION NUMBER: 168,190  
; FILING DATE: 15-MAR-1988  
; APPLICATION NUMBER: 54,369  
; FILING DATE: 26-MAY-1987  
; SEQ ID NO: 1:  
; LENGTH: 4383  
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QY 507 ATATATATATATATATATATATCGA 533  
DB 2413 ATATATATATATATATATATATCGA 2387

RESULT 11  
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; Sequence 34, Application US/09451651  
; Patent No. 6489101  
; GENERAL INFORMATION:  
; APPLICANT: DILLON, David Clifford  
; APPLICANT: Day, Craig Hilbing  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND DIAGNOSIS  
; FILE REFERENCE: 210121.491  
; CURRENT APPLICATION NUMBER: US/09/451,651  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 34  
; LENGTH: 432  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-451-651-34



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# RESULT 15

US-09-171-209-20  
Sequence 20, Application US/09171209  
Patent No. 6448000

## GENERAL INFORMATION:

APPLICANT: VANDERBILT UNIVERSITY  
305 Kirkland Hall  
Nashville, TN 37240

TITLE OF INVENTION: MAMMALIAN GENES INVOLVED IN VIRAL  
INFECTION

NUMBER OF SEQUENCES: 83

## CORRESPONDENCE ADDRESSES:

ADDRESSEE: Needle & Rosenberg, P.C.  
STREET: 127 Peachtree Street, Suite 1200  
CITY: Atlanta

STATE: Georgia  
COUNTRY: USA

ZIP: 30303-1811

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

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FILING DATE: 08-Mar-1999

CLASSIFICATION: <unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US97/06067  
FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Selby, Elizabeth

REGISTRATION NUMBER: 38,298  
REFERENCE/DOCKET NUMBER: 22000.0061/P

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404 688 0770

TELEFAX: 404 688 9880

INFORMATION FOR SEQ. ID NO: 20:

SEQUENCE CHARACTERISTICS:  
LENGTH: 888 base pairs

TYPE: nucleic acid  
STRANDEDNESS: double

TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
US-09-171-209-20

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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 780 GATATATATATATATATATATAT 804

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Job time: 83 secs

Tue Jul 6 09:07:33 2004

us-10-031-818b-1.oli.rmpb

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Comphen Ltd.

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Run on: July 4, 2004, 23:16:07 ; Search time 445 Seconds  
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Title: US-10-031-818b-1

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18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*  
19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	3.5	3528	9	US-09-777-347-2
2	27	3.5	3528	9	US-09-777-347-2
3	27	3.5	6526	15	US-10-311-455-2209
4	27	3.5	6526	15	US-10-311-455-2209
5	26	3.4	207	17	US-10-437-963-79690
6	26	3.4	207	17	US-10-437-963-79690
7	26	3.4	404	13	US-10-424-599-60831
8	26	3.4	404	13	US-10-424-599-60831
9	26	3.4	419	13	US-10-424-599-100147
10	26	3.4	419	13	US-10-424-599-100147
11	26	3.4	440	13	US-10-424-599-95178
12	26	3.4	440	13	US-10-424-599-95178
13	26	3.4	506	17	US-10-437-963-94087
14	26	3.4	506	17	US-10-437-963-94087

15	26	3.4	549	10	US-09-991-936-1818	Sequence 1818, Ap
16	26	3.4	549	10	US-09-991-936-1818	Sequence 1818, Ap
17	26	3.4	623	17	US-10-437-963-61122	Sequence 61122, A
18	26	3.4	623	17	US-10-437-963-61122	Sequence 61122, A
19	26	3.4	1079	17	US-10-437-963-80924	Sequence 80924, A
20	26	3.4	1079	17	US-10-437-963-80924	Sequence 80924, A
21	26	3.4	1218	17	US-10-437-963-92758	Sequence 92758, A
22	26	3.4	1218	17	US-10-437-963-92758	Sequence 92758, A
23	26	3.4	1461	9	US-09-938-842A-3207	Sequence 3207, Ap
24	26	3.4	1461	9	US-09-938-842A-3207	Sequence 3207, Ap
25	26	3.4	1461	11	US-09-938-842A-3207	Sequence 3207, Ap
26	26	3.4	1461	11	US-09-938-842A-3207	Sequence 3207, Ap
27	26	3.4	2000	9	US-09-938-842A-2951	Sequence 2951, Ap
28	26	3.4	2000	9	US-09-938-842A-2951	Sequence 2951, Ap
29	26	3.4	2000	9	US-09-938-842A-4203	Sequence 4203, Ap
30	26	3.4	2000	9	US-09-938-842A-4203	Sequence 4203, Ap
31	26	3.4	2000	11	US-09-938-842A-2951	Sequence 2951, Ap
32	26	3.4	2000	11	US-09-938-842A-2951	Sequence 2951, Ap
33	26	3.4	2000	11	US-09-938-842A-4203	Sequence 4203, Ap
34	26	3.4	2000	11	US-09-938-842A-4203	Sequence 4203, Ap
35	26	3.4	3559	13	US-08-892-635A-18	Sequence 18, Appl
36	26	3.4	3559	13	US-08-892-635A-18	Sequence 18, Appl
37	26	3.4	24023	14	US-10-094-679-1	Sequence 1, Appl1
38	26	3.4	24023	14	US-10-094-679-1	Sequence 1, Appl1
39	26	3.4	33675	9	US-09-921-992-2	Sequence 2, Appl1
40	26	3.4	33675	9	US-09-921-992-2	Sequence 2, Appl1
41	26	3.4	330973	13	US-10-087-192-1498	Sequence 1498, Ap
42	26	3.4	330973	13	US-10-087-192-1498	Sequence 1498, Ap
43	26	3.4	1503841	9	US-09-795-668-1	Sequence 1, Appl1
44	26	3.4	1503841	9	US-09-795-668-1	Sequence 1, Appl1
45	26	3.4	1503841	9	US-09-795-668-1	Sequence 1, Appl1

# ALIGNMENTS

RESULT 1  
US-09-777-347-2  
Sequence 2, Appl1  
Patent No. US20010014977A1  
GENERAL INFORMATION:  
APPLICANT: McBride, Kevin B.  
TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESS: Calgene, Inc.  
STREET: 1920 Fifth Street  
CITY: Davis  
STATE: CA  
COUNTRY: USA  
ZIP: 95616  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB  
OPERATING SYSTEM: Macintosh 7.1  
SOFTWARE: Microsoft Word 5.1 (a)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/777,347  
FILING DATE: 05-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/487,087  
FILING DATE: <Unknown>  
APPLICATION NUMBER: USSN 07/554,195  
FILING DATE: 17-JUL-90  
APPLICATION NUMBER: USSN 07/382,518  
FILING DATE: 19-JUL-89  
ATTORNEY/AGENT INFORMATION:  
NAME: Carl J. Schwedler  
REGISTRATION NUMBER: 36,924  
REFERENCE/DOCKET NUMBER: CGNE 91-1  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (916) 753-6313  
TELEFAX: (916) 753-1510  
INFORMATION FOR SEQ ID NO: 2  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3528 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 2  
US-09-777-347-2

Query Match 3.5%; Score 27; DB 9; Length 3528;  
Best Local Similarity 100.0%; Pred. No. 0.058; Indels 0; Gaps 0;  
Matches 27; Conservative 0; Mismatches 0;

QY 504 TCGATATATATATATATATATATAT 530  
DB 2387 TCGATATATATATATATATATATAT 2413

RESULT 2  
US-09-777-347-2/c  
Sequence 2, Application US/09777347  
Patent No. US2001001497A1  
GENERAL INFORMATION:  
APPLICANT: MGBride, Kevin E.  
TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Calgene, Inc.  
STREET: 1920 Fifth Street  
CITY: Davis  
STATE: CA  
COUNTRY: USA  
ZIP: 95616

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 7.1  
SOFTWARE: Microsoft Word 5.3 (a)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/777,347  
FILING DATE: 05-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/487,087  
FILING DATE: <Unknown>  
APPLICATION NUMBER: USSN 07/554,195  
FILING DATE: 17-JUL-90  
APPLICATION NUMBER: USSN 07/382,518  
FILING DATE: 19-JUL-89  
ATTORNEY/AGENT INFORMATION:  
NAME: Carl J. Schwedler  
REGISTRATION NUMBER: 36,924  
REFERENCE/DOCKET NUMBER: CGNE 91-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (916) 753-6313  
TELEFAX: (916) 753-1510  
INFORMATION FOR SEQ ID NO: 2  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3528 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 2  
US-09-777-347-2

Query Match 3.5%; Score 27; DB 9; Length 3528;  
Best Local Similarity 100.0%; Pred. No. 0.058; Indels 0; Gaps 0;  
Matches 27; Conservative 0; Mismatches 0;

QY 507 ATATATATATATATATATATATATCGA 533  
DB 2413 ATATATATATATATATATATATCGA 2387

RESULT 3  
US-10-311-455-2209  
Sequence 2209, Application US/10311455  
Publication No. US20030143606A1  
GENERAL INFORMATION:  
APPLICANT: OLEK, Alexander  
APPLICANT: PIEPENBROCK, Christian  
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Det  
TITLE OF INVENTION: Cytosine methylation  
FILE REFERENCE: 5013.1014  
CURRENT APPLICATION NUMBER: US/10/311,455  
CURRENT FILING DATE: 2002-12-16  
PRIOR APPLICATION NUMBER: PCT/EP01/07537  
PRIOR FILING DATE: 2001-07-02  
PRIOR APPLICATION NUMBER: DE 10032529.7  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: DE 10043826.1  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 2424  
SEQ ID NO 2209  
LENGTH: 6526  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-311-455-2209

Query Match 3.5%; Score 27; DB 15; Length 6526;  
Best Local Similarity 100.0%; Pred. No. 0.062; Indels 0; Gaps 0;  
Matches 27; Conservative 0; Mismatches 0;

QY 504 TCGATATATATATATATATATATATAT 530  
DB 3500 TCGATATATATATATATATATATAT 3526

RESULT 4  
US-10-311-455-2209/c  
Sequence 2209, Application US/10311455  
Publication No. US20030143606A1  
GENERAL INFORMATION:  
APPLICANT: OLEK, Alexander  
APPLICANT: PIEPENBROCK, Christian  
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Det  
TITLE OF INVENTION: Cytosine methylation  
FILE REFERENCE: 5013.1014  
CURRENT APPLICATION NUMBER: US/10/311,455  
CURRENT FILING DATE: 2002-12-16  
PRIOR APPLICATION NUMBER: PCT/EP01/07537  
PRIOR FILING DATE: 2001-07-02  
PRIOR APPLICATION NUMBER: DE 10032529.7  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: DE 10043826.1  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 2424  
SEQ ID NO 2209  
LENGTH: 6526  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-311-455-2209

Query Match 3.5%; Score 27; DB 15; Length 6526;  
Best Local Similarity 100.0%; Pred. No. 0.062; Indels 0; Gaps 0;



Matches: 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 507 ATATATATATATATATATATATCGA 533  
DB 3526 ATATATATATATATATATATATCGA 3500

## RESULT 5

US-10-437-963-79690  
; Sequence 79690, Application US/10437963  
; Publication No. US2004012343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Soukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 79690  
; LENGTH: 207  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_79386C.1  
US-10-437-963-79690

Query Match 3.4%; Score 26; DB 17; Length 207;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 507 ATATATATATATATATATATCG 532  
DB 10 ATATATATATATATATATATCG 35

## RESULT 6

US-10-437-963-79690/c  
; Sequence 79690, Application US/10437963  
; Publication No. US2004012343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Soukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 79690  
; LENGTH: 207  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_79386C.1  
US-10-437-963-79690

Query Match 3.4%; Score 26; DB 17; Length 207;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 505 CGATATATATATATATATATATAT 530

DB 35 CGATATATATATATATATATATAT 10

## RESULT 7

US-10-424-599-60831  
; Sequence 60831, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 60831  
; LENGTH: 404  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_25943C.1  
US-10-424-599-60831

Query Match 3.4%; Score 26; DB 13; Length 404;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 505 CGATATATATATATATATATATAT 530  
DB 11 CGATATATATATATATATATATAT 36

## RESULT 8

US-10-424-599-60831/c  
; Sequence 60831, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 60831  
; LENGTH: 404  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_25943C.1  
US-10-424-599-60831

Query Match 3.4%; Score 26; DB 13; Length 404;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 507 ATATATATATATATATATATATCG 532  
DB 36 ATATATATATATATATATATATCG 11

## RESULT 9

US-10-424-599-100147  
; Sequence 100147, Application US/10424599

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; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 100147
; LENGTH: 419
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_61448C.1
US-10-424-599-100147
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```
Query Match          3.4%; Score 26; DB 13; Length 419;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 505 CGATTATATATATATATATATATAT 530
Db 62 CGATTATATATATATATATATATAT 87
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RESULT 10
US-10-424-599-100147/C
; Sequence 100147, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 100147
; LENGTH: 419
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_61448C.1
US-10-424-599-100147
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Query Match          3.4%; Score 26; DB 13; Length 419;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 507 ATATATATATATATATATATATATCG 532
Db 87 ATATATATATATATATATATATATCG 62
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RESULT 11
US-10-424-599-95178
; Sequence 95178, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
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; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 95178
; LENGTH: 440
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_56959C.1
US-10-424-599-95178
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Query Match          3.4%; Score 26; DB 13; Length 440;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Oy 505 CGATTATATATATATATATATATAT 530
Db 11 CGATTATATATATATATATATATAT 36
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RESULT 12
US-10-424-599-95178/C
; Sequence 95178, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 95178
; LENGTH: 440
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_56959C.1
US-10-424-599-95178
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Query Match          3.4%; Score 26; DB 13; Length 440;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 507 ATATATATATATATATATATATATCG 532
Db 36 ATATATATATATATATATATATATCG 11
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RESULT 13
US-10-437-963-94087
; Sequence 94087, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 94087
; LENGTH: 506
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Page 5

TYPE: DNA  
ORGANISM: Oryza sativa  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT4530\_92409C.1  
US-10-437-963-94087

Query Match 3.4%; Score 26; DB 17; Length 506;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 507 ATATATATATATATATATATATCG 532  
DB 34 ATATATATATATATATATATATCG 59

RESULT 14  
US-10-437-963-94087/C  
Sequence 94087, Application US/10437963  
Publication No. US2004012343A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
APPLICANT: Wu, Wei  
APPLICANT: Boukharov, Andrey A.  
APPLICANT: Barbazuk, Brad  
APPLICANT: Li, Ping  
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53221)B  
CURRENT APPLICATION NUMBER: US/10/437,963  
CURRENT FILING DATE: 2003-05-14  
NUMBER OF SEQ ID NOS: 204966  
SEQ ID NO 94087  
LENGTH: 506  
TYPE: DNA  
ORGANISM: Oryza sativa  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT4530\_92409C.1  
US-10-437-963-94087

Query Match 3.4%; Score 26; DB 17; Length 506;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 505 CGATATATATATATATATATATAT 530  
DB 59 CGATATATATATATATATATATAT 34

RESULT 15  
US-09-991-936-1818  
Sequence 1818, Application US/09991936  
Publication No. US20030073827A1  
GENERAL INFORMATION:  
APPLICANT: Brandt, Kevin S.  
APPLICANT: Gaines, Patrick J.  
APPLICANT: Stinchcomb, Dan T.  
APPLICANT: Wisniewski, Nancy  
TITLE OF INVENTION: FLEA HEAD, NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF  
FILE REFERENCE: FC-6-C1  
CURRENT APPLICATION NUMBER: US/09/991,936  
CURRENT FILING DATE: 2001-11-21  
PRIOR APPLICATION NUMBER: US/09/543,668  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: 60/128,704  
PRIOR FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 1959  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 1818  
LENGTH: 549

TYPE: DNA  
ORGANISM: Ctenocephalides felis  
US-09-991-936-1818

Query Match 3.4%; Score 26; DB 10; Length 549;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 507 ATATATATATATATATATATATCG 532  
DB 491 ATATATATATATATATATATATCG 516

Search completed: July 5, 2004, 01:09:04  
Job time : 448 secs